GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:37:26 ; Search time 156 Seconds
(without alignments)
726.657 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VVLTIISLIILIMLWQKKPR 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 1596664

Minimum DB seq length: 0
Maximum DB seq length: 316

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1622	100.0	316	2	AAY32086	Aay32086 Single ch
2	1319	81.3	255	3	AAB11398	Aab11398 E. coli e
3	1319	81.3	255	4	AAB74199	Aab74199 PelB-scFv
4	1319	81.3	255	4	AAB70769	Aab70769 Expressio
5	1319	81.3	255	4	AAY72020	Aay72020 E. caroto
6	1237	76.3	241	6	ABR62010	Abr62010 Single-ch
7	1227	75.6	241	5	AAM48925	Aam48925 scFv anti
8	1194	73.6	236	2	AAR32842	Aar32842 VH NQ10/1
9	1185	73.1	240	2	AAR68613	Aar68613 Single ch
10	1097.5	67.7	223	2	AAR32841	Aar32841 VH NQ10/1
11	976.5	60.2	237	7	AAE38657	Aae38657 Mouse G1
12	970.5	59.8	268	3	AAY44973	Aay44973 Recombina
13	967.5	59.6	268	3	AAY44972	Aay44972 Recombina
14	964.5	59.5	284	2	AAR95569	Aar95569 Intracell
15	959	59.1	291	8	ADN06993	Adn06993 Human EFG
16	954	58.8	280	6	ABR42055	Abr42055 Newcastle
17	939	57.9	234	2	AAR64819	Aar64819 OMVU10 Sc
18	938.5	57.9	235	2	AAR32840	Aar32840 VH NQ2/12
19	937.5	57.8	272	8	ADO19054	Ado19054 Human ant
20	937	57.8	258	2	AAW90221	Aaw90221 Anti-B7.1
21	935.5	57.7	294	4	AAB20442	Aab20442 Anti-FIX/
22	934.5	57.6	293	4	AAG65715	Aag65715 Amino aci
23	928.5	57.2	282	6	ABJ19276	Abj19276 Anti-huma
24	927	57.2	291	8	ADN06992	Adn06992 Human EFG
25	926	57.1	287	8	ADN06988	Adn06988 Human EFG
26	921.5	56.8	244	8	ADQ75290	Adq75290 Immunoglo
27	913	56.3	242	6	ABR62132	Abr62132 Single ch
28	912	56.2	242	8	ADQ75289	Adq75289 Immunoglo
29	906.5	55.9	237	5	ABP46093	Abp46093 Human BLy
30	906.5	55.9	237	7	ADG96920	Adg96920 Single ch
31	906.5	55.9	253	2	AAW90225	Aaw90225 Anti-B7.1
32	903.5	55.7	237	5	ABP46009	Abp46009 Human BLy
33	903.5	55.7	237	7	ADG96836	Adg96836 Single ch
34	900.5	55.5	237	5	ABP46103	Abp46103 Human BLy
35	900.5	55.5	237	5	ABP45994	Abp45994 Human BLy
36	900.5	55.5	237	7	ADG96930	Adg96930 Single ch
37	900.5	55.5	237	7	ADG96821	Adg96821 Single ch
38	900.5	55.5	281	2	AAW82744	Aaw82744 Fusion pr
39	900	55.5	246	8	ADH50847	Adh50847 SGV RFB4
40	899.5	55.5	237	5	ABP46107	Abp46107 Human BLy
41	899.5	55.5	237	7	ADG96934	Adg96934 Single ch
42	898.5	55.4	237	5	ABP46104	Abp46104 Human BLy
43	898.5	55.4	237	7	ADG96931	Adg96931 Single ch
44	897.5	55.3	237	5	ABP46100	Abp46100 Human BLy
45	897.5	55.3	237	5	ABP46016	Abp46016 Human BLy

ALIGNMENTS

RESULT 1
AAY32086
ID AAY32086 standard; protein; 316 AA.
XX
AC AAY32086;
XX
DT 17-JAN-2000 (first entry)
XX
DE Single chain antibody used in probe detection.
XX
KW Single chain antibody; scAb; sFv; spectroscopic probe.
XX
OS Unidentified.
XX
PN WO9951986-A1.
XX
PD 14-OCT-1999.
XX
PF 08-APR-1999; 99WO-US007847.
XX
PR 08-APR-1998; 98US-0081118P.
PR 09-APR-1998; 98US-0081340P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Farinas J;
XX
DR WPI; 1999-611066/52.
DR N-PSDB; AAZ20266.
XX
PT Localizing probes to specific sites in cells that express single-chain
PT antibody reactive with probe-ligand conjugate, particularly for detecting
PT post-translational modification and its modulators.
XX
PS Claim 5; Page 47-48; 69pp; English.
XX
CC The present sequence represents a single chain antibody (scAb) that has 2
CC c-myc epitopes. The scAb is used in claimed methods for localizing a
CC probe and for detecting a post-translational activity in a cell, and is
CC expressed by a claimed transgenic non-human animal. The invention
CC provides methods and reagents for targeting probes to selected cellular
CC locations through the expression of specific binding partners (such as
CC scAbs) within a cell, and for creating assays for post-translational
CC activities. The invention allows the monitoring of the location of such
CC intracellular, specific binding patrtners over time and in response to
CC stimuli, such as test chemicals. Spectroscopic probes can be used to
CC screen a test chemical for activity. The invention also includes cells
CC and transgenic organisms comprising the intracellular specific binding

CC partner, where the specific binding partner can bind with the
CC spectroscopic probe/ligand conjugate. scAbs can be expressed within the
CC cell and can be designed to bind a wide variety of spectroscopic probes,
CC including small molecules that have better (and more diverse)
CC spectroscopic properties than green fluorescent protein
XX
SQ Sequence 316 AA;

Query Match 100.0%; Score 1622; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.6e-108;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGAVDEQKLISEEDLNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AEQKLISEEDLNGAVDEQKLISEEDLNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLT 300

Qy        301 IISLIILIMLWQKKPR 316
              ||||||||||||||||
Db        301 IISLIILIMLWQKKPR 316
```

RESULT 2
AAB11398
ID AAB11398 standard; protein; 255 AA.
XX
AC AAB11398;
XX
DT 22-FEB-2001 (first entry)
XX
DE E. coli expression plasmid pUBS520-ScFvOx encoded protein.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
KW disulfide bridge.
XX
OS Escherichia coli.
OS Synthetic.
XX
PN EP1048732-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-1999; 99EP-00107412.
XX
PR 26-APR-1999; 99EP-00107412.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
DR WPI; 2000-674185/66.
DR N-PSDB; AAC66074.
XX
PT Preparation of water-soluble eukaryotic polypeptides with disulfide
PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the
PT presence of arginine or amide compound.
XX
PS Example 6; Page 22-23; 40pp; German.
XX
CC This invention describes a novel preparation of a water-soluble,
CC naturally occurring eukaryotic polypeptide containing two or more
CC cysteine units bound via a disulfide bridge which comprises cultivation
CC of prokaryotic cells in the presence of arginine or an amide compound.
CC The method is useful for the preparation of eukaryotic proteins e.g.
CC proteases, interferons, protein hormones, antibodies or antibody
CC fragments (e.g. a single chain FV fragment that binds to thyroid
CC stimulating hormone). It is especially useful for preparing proteins with
CC more than five disulfide bridges, e.g. recombinant plasminogen activator
CC (rPA). The technique is simple and does not require in vitro after-
CC treatment, such as the removal of inclusion bodies, reduction or
CC naturization
XX
SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 3; Length 255;
Best Local Similarity 99.2%; Pred. No. 1.1e-86;
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
              ||||||||||||||
Db        241 AEQKLISEEDLNGA 254
```

RESULT 3
AAB74199
ID AAB74199 standard; protein; 255 AA.
XX
AC AAB74199;
XX
DT 29-MAY-2001 (first entry)
XX
DE PelB-scFvOxazolon fusion protein.
XX
KW Molecular chaperone; PelB signal sequence; scFvOxazolon.
XX
OS Unidentified.
XX
PN EP1077262-A1.
XX
PD 21-FEB-2001.
XX
PF 24-JUL-2000; 2000EP-00115839.
XX
PR 29-JUL-1999; 99EP-00114811.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX
DR WPI; 2001-246712/26.
DR N-PSDB; AAF77806.
XX
PT Producing naturally folded eukaryotic proteins e.g. antibodies,
PT interferon, hormones or proteases that contain two or several cysteines
PT linked by disulfide bridges comprises co-expression of a molecular
PT chaperone.
XX

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PS   Disclosure; Page 19; 35pp; English.
XX
CC   The present invention relates to a method for production of a naturally
CC   folded eukaryotic protein containing two or more cysteines linked by
CC   disulfide bridges. The method comprises co-expression and secretion into
CC   the periplasm of a molecular chaperone via an expression vector coding
CC   for the chaperone. The expression vector also encodes a signal sequence.
CC   The method is useful for producing a naturally folded eukaryotic protein
CC   such as an antibody, antibody fragment, interferon, protein hormone or a
CC   protease containing two or several cysteines linked by disulfide bridges.
CC   The present sequence is a fusion protein composed of the PelB signal
CC   sequence and ScFvOxazolon. This sequence was used in the method of the
CC   present invention
XX
SQ   Sequence 255 AA;

  Query Match             81.3%;  Score 1319;  DB 4;  Length 255;
  Best Local Similarity   99.2%;  Pred. No. 1.1e-86;
  Matches  252;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
              ||||||||||||||
Db        241 AEQKLISEEDLNGA 254


RESULT 4
AAB70769
ID   AAB70769 standard; protein; 255 AA.
XX
AC   AAB70769;
XX
DT   18-MAY-2001  (first entry)
XX
DE   Expression plasmid pUBS520-ScFvOx protein.
XX
KW   Chaperone protein; periplasm; antibody production; protein production;
KW   interferon production; protease production.
XX
OS   Escherichia coli.
OS   Synthetic.
XX
PN   EP1077263-A1.
XX
PD   21-FEB-2001.
XX
PF   29-JUL-1999;   99EP-00114811.
XX
PR   29-JUL-1999;   99EP-00114811.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
DR   WPI; 2001-204356/21.
DR   N-PSDB; AAF61193.
XX
PT   Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by
PT   simultaneous expression of a chaperone protein, allows simple recovery
PT   from periplasm or medium.
XX
PS   Disclosure; Page 20-21; 36pp; German.
XX
CC   This invention describes a novel method for preparing a naturally folded
CC   eukaryotic polypeptide (I) that contains two or more disulfide-bridged
CC   Cys residues by culturing prokaryotic cells that contain an expression
CC   vector for (I) including a prokaryotic signal sequence at its N-terminus
CC   and a nucleic acid (II) that secretes a chaperone protein (III) into the
CC   periplasm. (I) is secreted into the periplasm or medium; the signal
CC   peptide is then cleaved and (I) isolated from the periplasm or medium.
CC   The method is used for production of antibody, interferon, protein
CC   hormone or protease. Expression of (III) increases the yield of (I). The
CC   method is simple and eliminates time-consuming in vitro processing
CC   operations such as dissolution of inclusion bodies, reduction and
CC   refolding. (III) protects (I) against agglomeration and promotes their
CC   natural conformation
XX
SQ   Sequence 255 AA;

  Query Match             81.3%;  Score 1319;  DB 4;  Length 255;
  Best Local Similarity   99.2%;  Pred. No. 1.1e-86;
  Matches  252;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
              ||||||||||||||
Db        241 AEQKLISEEDLNGA 254


RESULT 5
AAY72020
ID   AAY72020 standard; protein; 255 AA.
XX
AC   AAY72020;
XX
DT   28-MAR-2001  (first entry)
XX
DE   E. carotovora PelB-scFvOx fusion protein encoded by pUBS520-pIN-scFvOx.
XX
KW   Secreted protein; chaperone; interferon; protease; hormone;
KW   naturally folded protein; lac promoter; DnaJ; heat shock protein; HSP;
KW   pectate lyase B; PelB; hapten; single-chain Fv-fragment Oxazolon;
KW   scFvOxazolon; fusion protein; thyroid stimulating hormone; TSH.
XX
OS   Pectobacterium carotovorum.
OS   Unidentified.
OS   Chimeric.
XX
PN   EP1054063-A2.
XX
PD   22-NOV-2000.
XX
PF   19-APR-2000; 2000EP-00108505.
XX
PR   26-APR-1999;   99EP-00107412.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
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PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;
XX
DR WPI; 2001-033777/05.
DR N-PSDB; AAD02212.
XX
PT Producing water-soluble, naturally folded, and secreted eukaryotic
PT polypeptide, involves culturing prokaryotic cells containing an
PT expression vector encoding the polypeptide in the presence of arginine or
PT a specific compound.
XX
PS Example 6; Page 22-23; 35pp; English.
XX
CC The patent discloses a method for the production of a water-soluble,
CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.
CC The method involves culturing the prokaryotic cells, containing an
CC expression vector encoding the desired protein and the prokaryotic signal
CC sequence, in the presence of an additive, e.g., L-arginine. The signal
CC sequence mediates the secretion of the desired protein into the
CC periplasm, where folding of the protein takes place. The prokaryotic cell
CC also contains an expression vector encoding a molecular chaperone, e.g.,
CC DnaJ and heat shock protein 25 (HSP25). The simultaneous co-
CC overexpression and co-secretion of molecular chaperones in the periplasm
CC improves the yield of functionally folded protein. The above method
CC recombinantly produces a high yield of eukaryotic secreted proteins in
CC prokaryotes. The method is useful for producing eukaryotic proteins such
CC as an antibody, antibody fragment, interferon, protein hormone or a
CC protease. The present sequence is an Erwinia carotovora pectate lyase B
CC (PelB) signal sequence-scFvOx fusion protein encoded by pUBS520-pIN-
CC scFvOx. The plasmid, pUBS520-pIN-scFvOx, also comprises the lac promoter.
CC The single-chain Fv-fragment, which is directed against the hapten
CC oxazolon (ScFvOxazolon), is an antibody fragment against thyroid
CC stimulating hormone (TSH). The co-expression of ScFvOx which has no
CC chaperone properties is used as a negative control
XX
SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;
Best Local Similarity 99.2%; Pred. No. 1.1e-86;
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
              ||||||||||||||
Db        241 AEQKLISEEDLNGA 254
```

RESULT 6
ABR62010
ID ABR62010 standard; protein; 241 AA.
XX
AC ABR62010;
XX
DT 03-OCT-2003 (first entry)
XX
DE Single-chain (scFv) antibody.
XX
KW Transgenic; biomolecule; ATP; ADP; cytostatic; virucide; gene therapy;
KW antisense therapy; scFv; antibody.
XX
OS Synthetic.
XX
PN EP1321524-A1.
XX
PD 25-JUN-2003.
XX
PF 19-DEC-2001; 2001EP-00130319.
XX
PR 19-DEC-2001; 2001EP-00130319.
XX
PA (DUER/) DUERING K.
XX
PI Mahn A, Hantke S, Petsch D;
XX
DR WPI; 2003-543829/52.
DR N-PSDB; ACC84876.
XX
PT Increasing the content of transgene-coded biomolecules in a plant or
PT animal, useful for producing proteins for diagnosing, preventing and/or
PT treating viral diseases and cancer, comprises changing the distribution
PT of ATP and/or ADP.
XX
PS Example 2; Fig 2; 18pp; English.
XX
CC The invention relates to increasing the content of one or more transgene-
CC coded biomolecules in an organism and involves changing the distribution
CC of ATP and/or ADP in cells of the organism. The yield of transgenic
CC molecules in host cells is often insufficient for industrial production.
CC The method increases the yield of transgenic molecules in animal and
CC plant host cells, therefore facilitating their production on an
CC industrial scale. The proteins produced by the method are useful for
CC diagnosing, preventing and/or treating viral diseases and cancer. The
CC present sequence represents a single-chain (scFv) antibody, used to
CC exemplify the increase in the expression of scFv antibodies in transgenic
CC potato tubers
XX
SQ Sequence 241 AA;

Query Match 76.3%; Score 1237; DB 6; Length 241;
Best Local Similarity 97.9%; Pred. No. 8.1e-81;
Matches 235; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 AEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIY 61
              |:|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ADVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIY 61

Qy         62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGS 121
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGGS 121

Qy        122 GGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDT 181
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        122 GGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDT 181

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
```

RESULT 7
AAM48925
ID AAM48925 standard; protein; 241 AA.
XX
AC AAM48925;
XX
DT 03-MAY-2002 (first entry)
XX
DE scFv antibody.
XX
KW Ketone binding protein; oxazole; pathogen resistance; virucide;
KW fungicide; antibacterial; scFv antibody.
XX

```
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 137
FT                   /note= "encoded by CAG"
FT   Misc-difference 201
FT                   /note= "encoded by TAC"
XX
PN   WO200204020-A2.
XX
PD   17-JAN-2002.
XX
PF   17-MAY-2001; 2001WO-DE001916.
XX
PR   12-JUL-2000; 2000DE-01033750.
XX
PA   (MPBC-) MPB COLOGNE GMBH.
XX
PI   Duering K,  Brinkmann O;
XX
DR   WPI; 2002-154868/20.
DR   N-PSDB; AAK98639.
XX
PT   Imparting pathogen resistance to plants and animals, comprises using a
PT   polypeptide that binds to an oxazole-derived ketone, optionally expressed
PT   from nucleic acid.
XX
PS   Example 3; Fig 1; 20pp; German.
XX
CC   The present invention relates to the use of a polypeptide that binds a
CC   ketone derived from oxazole for generating pathogen resistance in an
CC   organism. This can be used to impart resistance to pathogens (bacteria,
CC   fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,
CC   tobacco etc.), humans, farm animals and pets. Exemplified are activities
CC   against Phytophthora infestans and Erwinia carotovora in potatoes and
CC   Staphylococcus aureus in mice. The present sequence is a sc-Fv antibody,
CC   which is capable of binding 2-phenyloxazol-5-one
XX
SQ   Sequence 241 AA;

  Query Match             75.6%;  Score 1227;  DB 5;  Length 241;
  Best Local Similarity   97.1%;  Pred. No. 4.2e-80;
  Matches  234;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MADVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
              |||||||||||||||| |||||||||||:|||||||||||||||||||||||||||||||
Db        121 SGGGGSGGGGSDIELTGSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSVSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 A 241
              |
Db        241 A 241


RESULT 8
AAR32842
ID   AAR32842 standard; protein; 236 AA.
XX
AC   AAR32842;
XX
DT   25-MAR-2003  (revised)
DT   19-JUN-1993  (first entry)
XX
DE   VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences #2.
XX
KW   Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW   lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW   in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW   NQ2/12.4; NQ10/12.5.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .115
FT                   /label= VH_NQ10/12.5
FT   Peptide         116. .129
FT                   /note= "Linker peptide"
FT   Region          130. .236
FT                   /label= Vkappa_NQ10/12.5
XX
PN   WO9303151-A1.
XX
PD   18-FEB-1993.
XX
PF   10-AUG-1992;   92WO-GB001483.
XX
PR   10-AUG-1991;   91GB-00017352.
PR   11-JUN-1992;   92GB-00012419.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Embleton MJ,  Gorochov G,  Jones PT,  Winter GP;
XX
DR   WPI; 1993-076508/09.
DR   N-PSDB; AAQ37461.
XX
PT   Treatment of cell populations, partic. hybridomas - to link together
PT   copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
PS   Disclosure; Fig 4; 72pp; English.
XX
CC   The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC   and the Vk light chain genes of the antiphenyloxazolone hybridomas
CC   NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC   cell PCR. The cDNA encoding these peptides was synthesised using forward
CC   primers annealing to the Ck gene and the JH segment, followed by assembly
CC   with linker primers, VH back primers based on the VH3 leader sequence and
CC   a forward Ck primer nested in respect to the primer used for cDNA. The
CC   assembled product within the cells is then amplified with nested primers
CC   annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC   In-cell PCR may be used to determine gene linkage analysis, particularly
CC   for the cloning of gene combinations that are polymorphic within a
CC   population of cells, such as the rearranged genes for Ig or TCR V
CC   regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 236 AA;

  Query Match             73.6%;  Score 1194;  DB 2;  Length 236;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-78;
  Matches  226;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              |||||||||||||||||||||||||||| |||||||||||||||| ||||:||||||
Db         61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSAGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 182
              ||||||||  | ||||||||||||||:|||||||||||||||||||||||||||||||||
Db        121 GGGSGGGGSQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 180

Qy        183 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db        181 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 235

RESULT 9
AAR68613
ID   AAR68613 standard; protein; 240 AA.
XX
AC   AAR68613;
XX
DT   25-MAR-2003  (revised)
DT   13-SEP-1995  (first entry)
XX
DE   Single chain antibody (scFV) which binds to phenyloxazolone.
XX
KW   Genetic selection; ligand binding protein; cholera toxin; promoter;
KW   detection; selection; beta galactosidase; lac; transmembrane domain;
KW   regulatory domain; ds.
XX
OS   Synthetic.
XX
PN   DE4319296-A1.
XX
PD   15-DEC-1994.
XX
PF   10-JUN-1993;   93DE-04319296.
XX
PR   10-JUN-1993;   93DE-04319296.
XX
PA   (BEHW ) BEHRINGWERKE AG.
XX
PI   Fritz H,  Hennecke F,  Kolmar H;
XX
DR   WPI; 1995-023689/04.
DR   N-PSDB; AAQ80468.
XX
PT   Genetic selection of ligand binding proteins in microorganisms - by
PT   extracytoplasmic protein presentation, then use of ligand binding to
PT   express a detectable or selectable function.
XX
PS   Example 2.2; Fig 4; 25pp; German.
XX
CC   Genetic selection in microorganisms, for ligand binding proteins (LBP)
CC   comprises: extracytoplasmic presentation of LBP and; using the signal of
CC   ligand binding (by signal transduction on the biosynthetic machinery of
CC   the microorganisms) to express a detectable or selectable function.
CC   Microorganisms for this process include a genetically stable
CC   detection/selection and are transformed with a replicon encoding a fusion
CC   protein consisting of the LBP, a transmembrane helix and regulatory
CC   domain. The detection/selection function is expression of a beta-
CC   galactosidase gene, integrated into the chromosome and under the control
CC   of the ctx (cholera toxin) promoter. The transmembrane helix is taken
CC   from the toxR gene. Four primers (AAQ80457-60) were used in the
CC   construction of the plasmid pHKToxscFV. The primers described in AAQ80457
CC   -58 were used to amplify variable heavy chain sequence of the single
CC   chain antibody NQ10.12.5 and those described in AAQ80459-60 were used to
CC   amplify the corresponding light chain sequence from the same antibody.
CC   The amplified sequences were cloned into the plasmid pHKToxREI (See
CC   AAQ80454-56 for details) to create a toxR-scFV fusion gene. This sequence
CC   is the single chain antibody (scFV). (Updated on 25-MAR-2003 to correct
CC   PN field.)
XX
SQ   Sequence 240 AA;

  Query Match           73.1%;  Score 1185;  DB 2;  Length 240;
  Best Local Similarity  95.7%;  Pred. No. 4.4e-77;
  Matches  225;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA 63
              |:| | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 VQLVELGGGFVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA 65

Qy         64 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSGG 123
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||

Db         66 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSSGGGGSGG 125

Qy        124 GGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSK 183
              |||||||| | |||||||||||||:|||||||||||||||||||||||||| |||||
Db        126 GGSGGGGSQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWTYDTSK 185

Qy        184 LSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 LSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 240

RESULT 10
AAR32841
ID   AAR32841 standard; protein; 223 AA.
XX
AC   AAR32841;
XX
DT   25-MAR-2003  (revised)
DT   19-JUN-1993  (first entry)
XX
DE   VH NQ10/12.5-Vk NQ10/12.5 linked peptide sequences.
XX
KW   Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
KW   lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
KW   in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
KW   NQ2/12.4; NQ10/12.5.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .114
FT                   /label= VH_NQ10/12.5
FT   Peptide         115. .116
FT                   /note= "Linker peptide"
FT   Region          117. .223
FT                   /label= Vkappa_NQ10/12.5
XX
PN   WO9303151-A1.
XX
PD   18-FEB-1993.
XX
PF   10-AUG-1992;   92WO-GB001483.
XX
PR   10-AUG-1991;   91GB-00017352.
PR   11-JUN-1992;   92GB-00012419.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Embleton MJ,  Gorochov G,  Jones PT,  Winter GP;
XX
DR   WPI; 1993-076508/09.
DR   N-PSDB; AAQ37460.
XX
PT   Treatment of cell populations, partic. hybridomas - to link together
PT   copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
PS   Disclosure; Fig 3; 72pp; English.
XX
CC   The sequences given in AAR32840-43 show the mature heavy chain VH domains
CC   and the Vk light chain genes of the antiphenyloxazolone hybridomas
CC   NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
CC   cell PCR. The cDNA encoding these peptides was synthesised using forward
CC   primers annealing to the Ck gene and the JH segment, followed by assembly
CC   with linker primers, VH back primers based on the VH3 leader sequence and
CC   a forward Ck primer nested in respect to the primer used for cDNA. The
CC   assembled product within the cells is then amplified with nested primers
CC   annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
CC   In-cell PCR may be used to determine gene linkage analysis, particularly
CC   for the cloning of gene combinations that are polymorphic within a
CC   population of cells, such as the rearranged genes for Ig or TCR V
CC   regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 223 AA;
```

```
  Query Match             67.7%;  Score 1097.5;  DB 2;  Length 223;
  Best Local Similarity   90.2%;  Pred. No. 7.6e-71;
  Matches  212;  Conservative    4;  Mismatches    6;  Indels   13;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              |||||||||||||||||||||||||||| |||||||||||||| ||||:
Db         61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSA------ 114

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 182
                    | | ||||||||||||||:||||||||||||||||||||||||||||||||||
Db        115 -------ASQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 167

Qy        183 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 237
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 222


RESULT 11
AAE38657
ID   AAE38657 standard; protein; 237 AA.
XX
AC   AAE38657;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Mouse G1 single chain Fv-recombinant antibody.
XX
KW   Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;
KW   viral infection; autoimmune disease; gene therapy; cytostatic; virucide;
KW   immunomodulator; mouse.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .118
FT                   /note= "VH domain"
FT   Region          31. .35
FT                   /note= "Complementarity determining region"
FT   Region          50. .66
FT                   /note= "Complementarity determining region"
FT   Region          99. .108
FT                   /note= "Complementarity determining region"
FT   Region          119. .234
FT                   /note= "Peptide linker"
FT   Domain          135. .237
FT                   /note= "VL domain"
FT   Region          158. .167
FT                   /note= "Complementarity determining region"
FT   Region          182. .189
FT                   /note= "Complementarity determining region"
FT   Region          222. .230
FT                   /note= "Complementarity determining region"
XX
PN   WO2003068201-A2.
XX
PD   21-AUG-2003.
XX
PF   11-FEB-2003; 2003WO-IL000105.
XX
PR   13-FEB-2002; 2002US-00073301.
XX
PA   (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI   Reiter Y,  Denkberg G;
XX
DR   WPI; 2003-689603/65.
DR   N-PSDB; AAD58607.
XX
PT   New isolated molecule comprising an antibody that binds with a human
PT   major histocompatibility complex (MHC) class I being complexed with a HLA
PT   -restricted antigen, useful for treating cancer, viral infection or
PT   autoimmune disease.
XX
PS   Claim 63; Fig 3a; 81pp; English.
XX
CC   The invention relates to an isolated molecule comprising an antibody
CC   specifically bindable with a binding affinity below 20 nanomolar to a
CC   human major histocompatibility complex (MHC) class I being complexed with
CC   a HLA-restricted antigen. The molecules, antibodies, and methods are
CC   useful for treating cancer, viral infection and an autoimmune disease.
CC   The invention is useful in gene therapy. The present sequence is mouse G1
CC   single chain Fv-recombinant antibody
XX
SQ   Sequence 237 AA;

  Query Match             60.2%;  Score 976.5;  DB 7;  Length 237;
  Best Local Similarity   78.9%;  Pred. No. 3.9e-62;
  Matches  187;  Conservative   18;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|||||||||||:|||| |||||||||||||:|| |||| |:| ||||| |||| |  ||
Db          1 QVKLQESGGGLVKPGGSLKLSCAASGFTFSSYGMSWVRQTPDKRLEWVATISSGGSYTYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD-----YGAYWGQGTTVTVSSG 117
               |:|||||||||| ||||:|||:||:|||| ||||||      |   ||||||||||||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARGNWEGWYFDVWGQGTTVTVSSG 120

Qy        118 GGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRW 177
              |||||||||||||:||||||||||||||||||||||||:||: |:||| |:|| :
Db        121 GGGSGGGGSGGGGSNIELTQSPAIMSASPGERVTMTCSASSSIRYIYWYQQKPGSSPRLL 180

Qy        178 IYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL 234
              ||||| :: ||| |||||||||||||: ||||||||||:||  | ||| ||||
Db        181 IYDTSNVAPGVPFRFSGSGSGTSYSLTINRMEAEDAATYYCQEWSGYPYTFGGGTKL 237


RESULT 12
AAY44973
ID   AAY44973 standard; protein; 268 AA.
XX
AC   AAY44973;
XX
DT   23-MAY-2000  (first entry)
XX
DE   Recombinant mouse anti-rotavirus antibody (Clone 22).
XX
KW   Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;
KW   VH; light chain variable region; VL; pCANTAB 5E vector; treatment;
KW   probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;
KW   immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          6. .116
FT                   /label= Mouse_Heavy_chain_variable_region
FT   Region          117. .152
FT                   /label= Linker_region
FT   Region          153. .250
FT                   /label= Mouse_Light_chain_variable_region
FT   Domain          254. .266
FT                   /label= E_tag_domain
FT                   /note= "Enables immunodetection and immunoaffinity
FT                   purification of the recombinant antibody"
XX
PN   WO200006764-A1.
XX
PD   10-FEB-2000.
XX
PF   29-JUL-1999;   99WO-US017296.
```

```
XX
PR   30-JUL-1998;   98US-0094697P.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Fahl WE,  Letchworth GJ,  Mueller GC,  Savage AK,  Loo D;
XX
DR   WPI; 2000-195315/17.
DR   N-PSDB; AAZ50509.
XX
PT   Composition for supplementing or replacing an immune response against
PT   gastrointestinal pathogens in e.g. newborn infants, comprises probiotic
PT   microorganisms expressing antibodies specific for the gastrointestinal
PT   pathogens.
XX
PS   Disclosure; Fig 2; 48pp; English.
XX
CC   The present sequence is the recombinant mouse anti-rotavirus antibody. It
CC   comprises of mouse heavy chain (VH) and light chain (VL) variable regions
CC   joined by a linker. The recombinant antibody encoding DNA is inserted
CC   into pCANTAB 5E expression vector (clone 22). The vector is used to
CC   transform probiotic bacteria like, Lactobacilli for expression and
CC   secretion of recombinant anti-rotavirus antibodies. The antibodies have
CC   antibacterial and antiviral activity. Antibody-expressing probiotic
CC   bacteria can be administered for treatment of gastrointestinal (GI) tract
CC   infections and to immunise neonates, humans or immunosuppressed/
CC   immunodeficient adults acutely exposed to a bolus of GI pathogen
XX
SQ   Sequence 268 AA;

  Query Match             59.8%;  Score 970.5;  DB 3;  Length 268;
  Best Local Similarity   74.7%;  Pred. No. 1.2e-61;
  Matches  186;  Conservative   24;  Mismatches   30;  Indels    9;  Gaps    3;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:||:||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db          6 MAQVQLQQSGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTL 65

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYG-------AYWGQGTTVT 113
              :|||||||||||||||||||||||||||||:|| ||||||:|         |||||| ||
Db         66 HYADTVKGRFTISRDNPKNTLFLQMTSLRSQDTAMYYCAR-WGNYPHYAMDYWGQGTRVT 124

Qy        114 VSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGT 172
              |||||||||||||||||||||||||  :||| || ||:|| || ::  |: |:||| |
Db        125 VSSGGGGSGGGGSGGGGSDIELTQSPTTLSASVGETVTITCRASENIYSYLAWYQQKQGK 184

Qy        173 SPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGT 232
              ||:  :|    |: |||:||||||||| :|| |:|:: ||   |||| :  :| ||||||
Db        185 SPQFLVYSAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFGNYYCQHYYGSPRTFGAGT 244

Qy        233 KLELKRAAA 241
              |||:|||||
Db        245 KLEIKRAAA 253


RESULT 13
AAY44972
ID   AAY44972 standard; protein; 268 AA.
XX
AC   AAY44972;
XX
DT   23-MAY-2000  (first entry)
XX
DE   Recombinant mouse anti-rotavirus antibody (Clone 11).
XX
KW   Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;
KW   VH; light chain variable region; VL; pCANTAB 5E vector; treatment;
KW   probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;
KW   immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.
XX
OS   Synthetic.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          6. .116
FT                   /label= Mouse_Heavy_chain_variable_region
FT   Region          117. .151
FT                   /label= Linker_region
FT   Region          152. .250
FT                   /label= Mouse_Light_chain_variable_region
FT   Domain          254. .266
FT                   /label= E_tag_domain
FT                   /note= "Enables immunodetection and immunoaffinity
FT                   purification of the recombinant antibody"
XX
PN   WO200006764-A1.
XX
PD   10-FEB-2000.
XX
PF   29-JUL-1999;   99WO-US017296.
XX
PR   30-JUL-1998;   98US-0094697P.
XX
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
PI   Fahl WE,  Letchworth GJ,  Mueller GC,  Savage AK,  Loo D;
XX
DR   WPI; 2000-195315/17.
DR   N-PSDB; AAZ50508.
XX
PT   Composition for supplementing or replacing an immune response against
PT   gastrointestinal pathogens in e.g. newborn infants, comprises probiotic
PT   microorganisms expressing antibodies specific for the gastrointestinal
PT   pathogens.
XX
PS   Disclosure; Fig 1; 48pp; English.
XX
CC   The present sequence is the recombinant mouse anti-rotavirus antibody. It
CC   comprises of mouse heavy chain (VH) and light chain (VL) variable regions
CC   joined by a linker. The recombinant antibody encoding DNA is inserted
CC   into pCANTAB 5E expression vector (clone 11). The vector is used to
CC   transform probiotic bacteria like, Lactobacilli for expression and
CC   secretion of recombinant anti-rotavirus antibodies. The antibodies have
CC   antibacterial and antiviral activity. Antibody-expressing probiotic
CC   bacteria can be administered for treatment of gastrointestinal (GI) tract
CC   infections and to immunise neonates, humans or immunosuppressed/
CC   immunodeficient adults acutely exposed to a bolus of GI pathogen
XX
SQ   Sequence 268 AA;

  Query Match             59.6%;  Score 967.5;  DB 3;  Length 268;
  Best Local Similarity   75.1%;  Pred. No. 2e-61;
  Matches  187;  Conservative   22;  Mismatches   31;  Indels    9;  Gaps    3;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
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Db          6 MAQVQLQQSGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTL 65

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYG-------AYWGQGTTVT 113
              :|||||||||||||||||||||||||||||:|| ||||||:|         |||||| ||
Db         66 HYADTVKGRFTISRDNPKNTLFLQMTSLRSQDTAMYYCAR-WGNYPHYAMDYWGQGTTVT 124

Qy        114 VSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGT 172
              ||| |||||||||||||||  |||||| :||| || ||:|| || ::  |: |:||| |
Db        125 VSSSGGGSGGGGSGGGGSDIVLTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGK 184

Qy        173 SPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGT 232
              ||:  :|    |: |||:||||||||| :|| |:|:: ||   |||| :   | ||||||
Db        185 SPQFLVYSAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFGNYYCQHYYGTPRTFGAGT 244

Qy        233 KLELKRAAA 241
              |||||||||
Db        245 KLELKRAAA 253


RESULT 14
```

```
AAR95569
ID   AAR95569 standard; protein; 284 AA.
XX
AC   AAR95569;
XX
DT   06-SEP-1996  (first entry)
XX
DE   Intracellular binding protein ScFv-ras.
XX
KW   Intracellular binding protein; fusion protein; heavy chain; light chain;
KW   variable region; ras; monoclonal antibody; linker; PelB leader sequence;
KW   PCR; polymerase chain reaction; amplification; expression vector; cancer;
KW   phagemid; mammalian cell; structural formation; epitope; vaccination;
KW   gene therapy; viral infection; virus.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Protein         28. .270
FT                   /note= "ScFv anti-ras"
FT   Region          148. .162
FT                   /note= "linker sequence"
XX
PN   WO9429446-A2.
XX
PD   22-DEC-1994.
XX
PF   15-JUN-1994;   94WO-FR000714.
XX
PR   16-JUN-1993;   93FR-00007241.
XX
PA   (RHON ) RHONE POULENC RORER SA.
XX
PI   Schweighoffer F,  Tocque B;
XX
DR   WPI; 1995-036475/05.
DR   N-PSDB; AAT27009.
XX
PT   Nucleic acid encoding intracellular binding protein - partic. antibody or
PT   deriv., under control of promoter functional in mammalian cells, for gene
PT   therapy of cancer and virus disease.
XX
PS   Example 1; Page 23-25; 32pp; French.
XX
CC   This is the amino acid sequence of a novel intracellular binding protein
CC   of the invention generated by fusing the heavy and light chains variable
CC   regions of the anti-ras monoclonal antibody Y13-259. The regions are
CC   separated by a linker sequence (GGGGS) X 3. The gene also contains a PelB
CC   leader sequence. The fusion protein was synthesised by PCR amplifying the
CC   Vh and Vk coding sequences and ligating them with the linker sequence
CC   into an expression vector such as a phagemid e.g. M13. The sequence can
CC   also be inserted into a mammalian cell for expression of the protein. The
CC   linker sequence confers sufficient flexibility to allow correct
CC   structural formation of the antibody fragments. The novel proteins are
CC   expressed intracellularly and can target epitopes not accessible by the
CC   usual vaccination methods. The protein can thus be used for gene therapy
CC   e.g. of cancer or viral infections
XX
SQ   Sequence 284 AA;

  Query Match             59.5%;  Score 964.5;  DB 2;  Length 284;
  Best Local Similarity   72.2%;  Pred. No. 3.5e-61;
  Matches  187;  Conservative   24;  Mismatches   41;  Indels    7;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:|||||||||| | ||||  ||||||::||:|:|| | |||||||||||||| :
Db         26 MAQVKLQQSGGGLVQPGRSLKLSCVVSGFTFSNYGMNWIRQTPGKGLEWVAYISSGSSYL 85

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR------DYGAYWGQGTTVTV 114
              |||:||||||||||| ||||:|||||||||| :|||||      |:  ||||||||||
Db         86 YYAETVKGRFTISRDNAKNTLYLQMTSLRSEDTALYYCARHEGTGTDFFDYWGQGTTVTV 145

Qy        115 SSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTS 173
              ||||||||||||||||||:|||||  :||| || |:: | ||  :  |: |:||| | |
Db        146 SSGGGGSGGGGSGGGGSDVELTQSPHSLSASLGETVSIECLASEGISNYLAWYQQKPGKS 205

Qy        174 PKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTK 233
              |: || | | |||:||||||||| :|| ||:|: ||   |||||    | |||||||
Db        206 PQLLIYYASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYYCQQAYKYPSTFGAGTK 265

Qy        234 LELKRAAAEQKLISEEDLN 252
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Db        266 LEIKRAAAEQKLISEEDLN 284


RESULT 15
ADN06993
ID   ADN06993 standard; protein; 291 AA.
XX
AC   ADN06993;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human EFGR bs-scFv antibody protein, EGFR.E8.
XX
KW   Bispecific single chain; bs-scFv; cancer;
KW   epidermal growth factor receptor; EGFR; therapy; antibody; human.
XX
OS   Homo sapiens.
XX
PN   US2004071696-A1.
XX
PD   15-APR-2004.
XX
PF   04-APR-2003; 2003US-00406830.
XX
PR   05-APR-2002; 2002US-0370276P.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (FOXC-) FOX CHASE CANCER CENT.
XX
PI   Adams GP,  Horak EM,  Weiner LM,  Marks JD;
XX
DR   WPI; 2004-328525/30.
XX
PT   Novel bispecific antibody comprising first and second antibody joined to
PT   each other and having binding specificity to different epitopes of
PT   Epidermal Growth Factor Receptor protein, useful for treating cancer.
XX
PS   Claim 14; SEQ ID NO 10; 57pp; English.
XX
CC   The present invention provides bispecific single chain (bs-scFv) antibody
CC   molecules which may be used to treat various forms of cancer associated
CC   with the overexpression of the epidermal growth factor receptor (EGFR)
CC   family. The invention is useful for specifically delivering an effector
CC   molecule to a cell bearing a receptor from EGFR protein family chosen
CC   from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
CC   treatment of cancer. The present sequence is human EFGR bs-scFv antibody
CC   protein.
XX
SQ   Sequence 291 AA;

  Query Match             59.1%;  Score 959;  DB 8;  Length 291;
  Best Local Similarity   70.1%;  Pred. No. 9e-61;
  Matches  185;  Conservative   31;  Mismatches   38;  Indels   10;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:|||||||:|||| | :|||||||||||: | |||||| ||||||: ||    :
Db         21 MAQVQLQESGGGMVQPGRSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGST 80

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD---------YGAYWGQGTT 111
              ||||:|||||||||| ||||:||| |||:||| :|||||:         |   ||:||
Db         81 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTALYYCAREGYSSNWNNWYFDLWGRGTL 140

Qy        112 VTVSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKS 170
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Db        141 VTVSSGGGGSGGGGSGGGGSEIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKP 200

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              | :||  ||  | | ||||:||||||||| ::|||||:: :| |||||||::| | |||
Db        201 GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYNSYPWTFGQ 260

Qy        231 GTKLELKRAAAEQKLISEEDLNGA 254
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Db        261 GTKLEIKRAAAEQKLISEEDLNGA 284
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Search completed: December 30, 2004, 15:51:37
Job time : 164 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:49:07 ; Search time 38 Seconds
(without alignments)
551.487 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VVLTIISLIILIMLWQKKPR 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 410336

Minimum DB seq length: 0
Maximum DB seq length: 316

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1319	81.3	255	3	US-09-553-498-8	Sequence 8, Appli
2	1319	81.3	255	4	US-09-618-869-8	Sequence 8, Appli
3	1199	73.9	236	2	US-08-190-199A-65	Sequence 65, Appl
4	1185	73.1	240	2	US-08-956-047-25	Sequence 25, Appl
5	1102.5	68.0	223	2	US-08-190-199A-63	Sequence 63, Appl
6	964.5	59.5	284	3	US-08-564-164A-2	Sequence 2, Appli
7	943.5	58.2	235	2	US-08-190-199A-61	Sequence 61, Appl
8	900.5	55.5	281	3	US-09-423-439-44	Sequence 44, Appl
9	897.5	55.3	245	4	US-09-138-091A-76	Sequence 76, Appl
10	894	55.1	240	4	US-09-192-854-2	Sequence 2, Appli
11	890.5	54.9	245	3	US-08-918-148-75	Sequence 75, Appl
12	890.5	54.9	245	3	US-08-918-148-78	Sequence 78, Appl
13	890.5	54.9	245	4	US-09-138-091A-73	Sequence 73, Appl
14	881.5	54.3	245	3	US-08-918-148-76	Sequence 76, Appl
15	881.5	54.3	245	4	US-09-138-091A-74	Sequence 74, Appl
16	877	54.1	270	2	US-08-652-507-2	Sequence 2, Appli
17	873.5	53.9	301	2	US-08-661-052-14	Sequence 14, Appl
18	873.5	53.9	301	3	US-09-188-082-14	Sequence 14, Appl
19	873.5	53.9	301	3	US-09-364-088-14	Sequence 14, Appl
20	873.5	53.9	301	3	US-09-102-716-14	Sequence 14, Appl
21	864	53.3	258	4	US-09-526-738A-4	Sequence 4, Appli
22	861	53.1	239	3	US-08-279-772A-8	Sequence 8, Appli
23	861	53.1	239	3	US-08-902-486-11	Sequence 11, Appl
24	861	53.1	282	2	US-08-860-174A-10	Sequence 10, Appl
25	858.5	52.9	284	3	US-09-184-658-40	Sequence 40, Appl
26	858.5	52.9	284	4	US-09-504-262D-40	Sequence 40, Appl
27	855	52.7	244	3	US-08-918-148-77	Sequence 77, Appl
28	855	52.7	244	4	US-09-138-091A-75	Sequence 75, Appl
29	855	52.7	256	4	US-09-526-738A-2	Sequence 2, Appli
30	853.5	52.6	242	2	US-08-553-497A-26	Sequence 26, Appl
31	851	52.5	246	1	US-08-469-486-57	Sequence 57, Appl
32	851	52.5	246	2	US-08-469-658-57	Sequence 57, Appl
33	847	52.2	222	2	US-08-190-199A-67	Sequence 67, Appl
34	840.5	51.8	244	2	US-08-553-497A-20	Sequence 20, Appl
35	838.5	51.7	242	2	US-08-553-497A-28	Sequence 28, Appl
36	836.5	51.6	244	2	US-08-553-497A-22	Sequence 22, Appl
37	834	51.4	310	3	US-09-079-029-11	Sequence 11, Appl
38	829	51.1	289	3	US-09-184-658-63	Sequence 63, Appl
39	829	51.1	289	4	US-09-504-262D-63	Sequence 63, Appl
40	828	51.0	239	2	US-08-553-497A-18	Sequence 18, Appl
41	819.5	50.5	246	2	US-08-553-497A-24	Sequence 24, Appl
42	815.5	50.3	267	3	US-09-485-737B-2	Sequence 2, Appli
43	813.5	50.2	240	1	US-08-488-113B-148	Sequence 148, App
44	813.5	50.2	240	1	US-08-477-484B-148	Sequence 148, App
45	813.5	50.2	240	2	US-08-646-360-148	Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-553-498-8
; Sequence 8, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-8

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Best Local Similarity 99.2%; Pred. No. 8e-91;
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
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Db        241 AEQKLISEEDLNGA 254
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RESULT 2
US-09-618-869-8
; Sequence 8, Application US/09618869

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; Patent No. 6455279
; GENERAL INFORMATION:
;  APPLICANT:  Ambrosius, Dorthee
;  APPLICANT:  Rudolph, Rainer
;  APPLICANT:  Schaeffner, Joerg
;  APPLICANT:  Schwarz, Elisabeth
;  TITLE OF INVENTION:  PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
;  TITLE OF INVENTION:  SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
;  TITLE OF INVENTION:  CHAPERONES
;  FILE REFERENCE:  20381
;  CURRENT APPLICATION NUMBER: US/09/618,869
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER:  EP99114811.5
;  PRIOR FILING DATE:  1999-07-29
;  NUMBER OF SEQ ID NOS:  10
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-09-618-869-8

  Query Match             81.3%;  Score 1319;  DB 4;  Length 255;
  Best Local Similarity   99.2%;  Pred. No. 8e-91;
  Matches  252;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGG 120
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTTVTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
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Db        121 SGGGGSGGGGSDIELTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180

Qy        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240
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Db        181 TSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAA 240

Qy        241 AEQKLISEEDLNGA 254
              ||||||||||||||
Db        241 AEQKLISEEDLNGA 254


RESULT 3
US-08-190-199A-65
; Sequence 65, Application US/08190199A
; Patent No. 5830663
;  GENERAL INFORMATION:
;    APPLICANT:  EMBLETON, Michael J.
;    APPLICANT:  GOROCHOV, Guy
;    APPLICANT:  JONES, Peter T.
;    APPLICANT:  WINTER, Gregory P.
;    TITLE OF INVENTION:  TREATMENT OF CELL POPULATIONS
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,199A
;      FILING DATE:  13-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/01483
;      FILING DATE:  10-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9212419.7
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9117352.6
;      FILING DATE:  10-AUG-1991
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  236 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-190-199A-65

  Query Match             73.9%;  Score 1199;  DB 2;  Length 236;
  Best Local Similarity   96.2%;  Pred. No. 6.3e-82;
  Matches  227;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||:||||||
Db         61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSAGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 182
              ||||||||| | |||||||||||||:||||||||||||||||||||||||||||||||||
Db        121 GGGSGGGGSQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 180

Qy        183 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 236


RESULT 4
US-08-956-047-25
; Sequence 25, Application US/08956047
; Patent No. 5882924
;  GENERAL INFORMATION:
;    APPLICANT:  Fritz, Hans-Joachim
;    APPLICANT:  Hennecke, Frank
;    APPLICANT:  Kolmar, Harald
;    TITLE OF INVENTION:  Genetic Selection, by Means of Signal
;    TITLE OF INVENTION:  Transduction in Microorganisms, of Proteins Which are
;    TITLE OF INVENTION:  Capable of Ligand Binding
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett & Dunner
;      STREET:  1300 I Street, N.W., Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/956,047
;      FILING DATE:  22-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/257,669
;      FILING DATE:  08-JUN-1994
;      APPLICATION NUMBER:  DE P 43 19 296.3
;      FILING DATE:  10-JUN-1993
;      CLASSIFICATION:  435
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pohlman, Sandra M.
;      REGISTRATION NUMBER:  P39,691
;      REFERENCE/DOCKET NUMBER:  05552.1368-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-956-047-25

  Query Match             73.1%;  Score 1185;  DB 2;  Length 240;
  Best Local Similarity   95.7%;  Pred. No. 7.1e-81;
  Matches  225;  Conservative    2;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          4 VKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA 63
              |:| | ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 VQLVELGGGFVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA 65

Qy         64 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSGG 123
              |||||||||||||||||||||||||||| |||||||||||||| ||||||||||||
Db         66 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSSGGGGSGG 125

Qy        124 GGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSK 183
              |||||||| | |||||||||||||:|||||||||||||||||||||||| |||||
Db        126 GGSGGGGSQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWTYDTSK 185

Qy        184 LSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 LSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 240


RESULT 5
US-08-190-199A-63
; Sequence 63, Application US/08190199A
; Patent No. 5830663
;  GENERAL INFORMATION:
;    APPLICANT:  EMBLETON, Michael J.
;    APPLICANT:  GOROCHOV, Guy
;    APPLICANT:  JONES, Peter T.
;    APPLICANT:  WINTER, Gregory P.
;    TITLE OF INVENTION:  TREATMENT OF CELL POPULATIONS
;    NUMBER OF SEQUENCES:  70
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY MADISON & SUTRO, L.L.P.
;      STREET:  1100 New York Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/190,199A
;      FILING DATE:  13-JUL-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/01483
;      FILING DATE:  10-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9212419.7
;      FILING DATE:  11-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9117352.6
;      FILING DATE:  10-AUG-1991
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  223 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-190-199A-63

  Query Match             68.0%;  Score 1102.5;  DB 2;  Length 223;
  Best Local Similarity   90.3%;  Pred. No. 9.1e-75;
  Matches  213;  Conservative    4;  Mismatches    6;  Indels   13;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||||||||||||||||||||||||||||| |||||||||||||| ||||:
Db         61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARDYGAYWGQGTLVTVSA------ 114

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 182
                  | | |||||||||||||:|||||||||||||||||||||||||||||||
Db        115 -------ASQIVLTQSPAIMSASPGEKVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 167

Qy        183 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 223


RESULT 6
US-08-564-164A-2
; Sequence 2, Application US/08564164A
; Patent No. 6159947
;  GENERAL INFORMATION:
;    APPLICANT:  Schweighoffer, Fabien
;    APPLICANT:  Tocque, Bruno
;    TITLE OF INVENTION:  Intracellular Binding Proteins and Use
;    TITLE OF INVENTION:  Thereof
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426-0107
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/564,164A
;      FILING DATE:  28-DEC-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/FR94/00714
;      FILING DATE:  15-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 93/07241
;      FILING DATE:  16-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Savitzky, Martin F.
;      REGISTRATION NUMBER:  29,699
;      REFERENCE/DOCKET NUMBER:  ST93030-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610)454-3816
;      TELEFAX:  (610)454-3808
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  284 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
```

US-08-564-164A-2

Query Match 59.5%; Score 964.5; DB 3; Length 284;
Best Local Similarity 72.2%; Pred. No. 2.3e-64;
Matches 187; Conservative 24; Mismatches 41; Indels 7; Gaps 2;

```
Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:|||||||| | ||||  ||||||::||:|:|| | ||||||||||||| :
Db         26 MAQVKLQQSGGGLVQPGRSLKLSCVVSGFTFSNYGMNWIRQTPGKGLEWVAYISSGSSYL 85

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR------DYGAYWGQGTTVTV 114
              |||:|||||||||||| ||||:|||||||||| :|||||      |:  ||||||||||
Db         86 YYAETVKGRFTISRDNAKNTLYLQMTSLRSEDTALYYCARHEGTGTDFFDYWGQGTTVTV 145

Qy        115 SSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTS 173
              |||||||||||||||||:||||||  :||| || |:: | ||  :  |: |:||| | |
Db        146 SSGGGGSGGGGSGGGGSDVELTQSPHSLSASLGETVSIECLASEGISNYLAWYQQKPGKS 205

Qy        174 PKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTK 233
              |:  ||  | |  |||:|||||||| :|| ||:|: ||   |||||    | |||||||
Db        206 PQLLIYYASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYYCQQAYKYPSTFGAGTK 265

Qy        234 LELKRAAAEQKLISEEDLN 252
              ||:||||||||||||||||
Db        266 LEIKRAAAEQKLISEEDLN 284
```

RESULT 7
US-08-190-199A-61
; Sequence 61, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-190-199A-61

Query Match 58.2%; Score 943.5; DB 2; Length 235;
Best Local Similarity 75.0%; Pred. No. 6.7e-63;
Matches 177; Conservative 26; Mismatches 32; Indels 1; Gaps 1;

```
Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:|:||| ||| |  |  ::|  |||: :|:|:||||| | |||||:  | :| ||  |
Db          1 QVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAGGST-NY 59

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
                 :  | :||:|| |: :||:| ||:::|| |||||| |||||||| ||||:||||||
Db         60 NSALMSRLSISKDNSKSQVFLKMNSLQTDDTAMYYCARDRGAYWGQGTLVTVSAGGGGSG 119

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTS 182
              ||||||||| | |||||||||||||::|||||||||| ||:|:|||||||||||||||
Db        120 GGGSGGGGSQIVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTS 179

Qy        183 KLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||:|||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        180 KLASGVPARFSGSGSATSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 235
```

RESULT 8
US-09-423-439-44
; Sequence 44, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-No. 6339070-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44

Query Match 55.5%; Score 900.5; DB 3; Length 281;
Best Local Similarity 68.6%; Pred. No. 1.3e-59;
Matches 179; Conservative 24; Mismatches 43; Indels 15; Gaps 3;

```
Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||:||:||  ||: | | |||| ||||      ||||:| ||:||||:|:|   :
Db         21 MAEVQLQQSGAELVRSGASVKLSCTASGFNIKDNYMHWVKQRPEQGLEWIAWIDPENGDT 80

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYC---------ARDYGAYWGQGTT 111
              ||   :|: |:: |:  || :| ::|| |||| :|||          | |   ||||||:
Db         81 EYAPKFRGKATLTADSSSNTAYLHLSSLTSEDTAVYYCHVLIYAGYLAMD---YWGQGTS 137

Qy        112 VTVSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSG 171
              | |||||||||||||||| | ||||||||||||||:||:|||||||| ||:|||||  |
```

```
Db        138 VAVSSGGGGSGGGGSGGGGSQIVLTQSPAIMSASPGEKVTITCSASSSVTYMHWFQQKPG 197

Qy        172 TSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAG 231
              |||| ||| || |:||||||||||||||||||| |||||||||||| |: |||||||
Db        198 TSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSTYPLTFGAG 257

Qy        232 TKLELKRAAAEQKLISEEDLN 252
              ||||:||   ||||||||||
Db        258 TKLEIKR---EQKLISEEDLN 275


RESULT 9
US-09-138-091A-76
; Sequence 76, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia W.
;  APPLICANT:  Carter, Paul J.
;  APPLICANT:  Fendly, Brian M.
;  APPLICANT:  Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: 9491-013-27
;  CURRENT APPLICATION NUMBER: US/09/138,091A
;  CURRENT FILING DATE:  1998-08-21
;  PRIOR APPLICATION NUMBER: US 60/056,736
;  PRIOR FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: single chain antibody (scFv) fragments
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 208
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-138-091A-76

  Query Match             55.3%;  Score 897.5;  DB 4;  Length 245;
  Best Local Similarity   69.8%;  Pred. No. 1.9e-59;
  Matches  171;  Conservative   34;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:| |||||||:|||| :|||||||||||  |:|||||| ||||||: ||| || |
Db          1 MAQVQLVESGGGLVKPGGSLRLSCAASGFTFSSHNMNWVRQAPGKGLEWVSSISSSSSYI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGA----YWGQGTTVTVSS 116
              ||||:|||||||||| ||:|:||| |||:||| :|||||| |:     ||:|| |||||
Db         61 YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRGSTGMDVWGRGTLVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              |||||||||||||||::|||| :||| |:|||:|| ||  :  :: |:||| | :||
Db        121 GGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
              ||  | |:|| |:||||||||| :: ||||:: :| |||||||:|: |||||  |||||
Db        181 LLIYKASSLASGAPSRFSGSGSGTDFTXTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
              :||||
Db        241 IKRAA 245


RESULT 10
US-09-192-854-2
; Sequence 2, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-192-854-2

  Query Match             55.1%;  Score 894;  DB 4;  Length 240;
  Best Local Similarity   71.7%;  Pred. No. 3.3e-59;
  Matches  172;  Conservative   27;  Mismatches   37;  Indels    4;  Gaps    3;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              ||:| |||||||||||| :|||||||||||: | |||||| ||||||: ||     : ||
Db          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGA--YWGQGTTVTVSSGGGG 120
              ||:|||||||||||| ||||:||| |||:||| :||||: |||  |||||| |||||||||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKSYGAFDYWGQGTLVTVSSGGGG 120

Qy        121 SGGGGSGGGGS-DIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWI 178
              |||||||||||| ||::|||||: :||| |:|||:|| || |:  |:||:||| | :||  |
Db        121 SGGGGSGGGGSTDIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLI 180

Qy        179 YDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              |  | | |||||:||||||||| ::|||||:: || |||||||  | | ||| |||:|:||
Db        181 YAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPNTFGQGTKVEIKR 240


RESULT 11
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia
;  APPLICANT: W.
;  APPLICANT: Carter, Paul J.
;  APPLICANT: Fendly, Brian M.
;  APPLICANT: Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: P0979
;  CURRENT APPLICATION NUMBER: US/08/918,148A
;  CURRENT FILING DATE: 1997-08-25
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: artificial
US-08-918-148-75

  Query Match             54.9%;  Score 890.5;  DB 3;  Length 245;
  Best Local Similarity   69.4%;  Pred. No. 6.2e-59;
  Matches  170;  Conservative   31;  Mismatches   39;  Indels    5;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||:| :||||||:|||| :|||||||||||  : | |:|||| ||||||:|||| |||
Db          1 MAEVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR----DYGAYWGQGTTVTVSS 116
              ||||:|||||||||| |||||||| |||:||| :|||||     |    ||||| |||||
Db         61 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGEDAFDIWGQGTMVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              |||||||||||||||| :||||: :||| |:|| :|| ||  :  :: |:||| | :||
Db        121 GGGGSGGGGSGGGGSDIVMTQSPSTLSASVGDRVAITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
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Db        181 LLIYKASSLASGAPSRFSGSGSGADFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
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Db        241 VKRAA 245


RESULT 12
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia
;  APPLICANT: W.
;  APPLICANT: Carter, Paul J.
;  APPLICANT: Fendly, Brian M.
;  APPLICANT: Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: P0979
;  CURRENT APPLICATION NUMBER: US/08/918,148A
;  CURRENT FILING DATE: 1997-08-25
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: artificial
;   FEATURE:
;   NAME/KEY: unknown
;   LOCATION: 208
;   OTHER INFORMATION: unknown amino acid
US-08-918-148-78

  Query Match             54.9%;  Score 890.5;  DB 3;  Length 245;
  Best Local Similarity   69.4%;  Pred. No. 6.2e-59;
  Matches  170;  Conservative   34;  Mismatches   36;  Indels    5;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
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Db          1 MAQVQLVESGGGLVKPGGSLRLSCAASGFTFSSHNMNWVRQAPGKGLEWVSSISSSSSYI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGA----YWGQGTTVTVSS 116
              ||||:|||||||||| ||:|:||| |||:||| :|||||| |:      ||:|| |||||
Db         61 YYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRGSTGMDVWGRGTLVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
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Db        121 GGGGSGGGGSGGGGSKIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
                ||  | |:|| |:|||||||| :: ||||:: :| |||||||:|: ||||| |||||
Db        181 LLIYKASSLASGAPSRFSGSGSGTDFTXTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
                :||||
Db        241 IKRAA 245


RESULT 13
US-09-138-091A-73
; Sequence 73, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia W.
;  APPLICANT:  Carter, Paul J.
;  APPLICANT:  Fendly, Brian M.
;  APPLICANT:  Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: 9491-013-27
;  CURRENT APPLICATION NUMBER: US/09/138,091A
;  CURRENT FILING DATE:  1998-08-21
;  PRIOR APPLICATION NUMBER: US 60/056,736
;  PRIOR FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-73

  Query Match             54.9%;  Score 890.5;  DB 4;  Length 245;
  Best Local Similarity   69.4%;  Pred. No. 6.2e-59;
  Matches  170;  Conservative   31;  Mismatches   39;  Indels    5;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||:| :||||||:|||| :|||||||||||| : | |:|||| ||||||:|||| |||
Db          1 MAEVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTI 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR----DYGAYWGQGTTVTVSS 116
              ||||:|||||||||| ||||:||| |||:||| :|||||     |     ||||| |||||
Db         61 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGEDAFDIWGQGTMVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              |||||||||||||||| :||||: :||| |:||| :|| ||  :  :: |:||| | :||
Db        121 GGGGSGGGGSGGGGSDIVMTQSPSTLSASVGDRVAITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
                ||  | |:|| |:|||||||| ::|||||:: :| |||||||:|: ||||| |||||
Db        181 LLIYKASSLASGAPSRFSGSGSGADFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
                :||||
Db        241 VKRAA 245


RESULT 14
US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia
;  APPLICANT: W.
;  APPLICANT: Carter, Paul J.
;  APPLICANT: Fendly, Brian M.
;  APPLICANT: Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: P0979
;  CURRENT APPLICATION NUMBER: US/08/918,148A
;  CURRENT FILING DATE: 1997-08-25
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: artificial
US-08-918-148-76

  Query Match             54.3%;  Score 881.5;  DB 3;  Length 245;
  Best Local Similarity   68.2%;  Pred. No. 2.9e-58;
  Matches  167;  Conservative   33;  Mismatches   40;  Indels    5;  Gaps    2;

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              ||||:| :||||:||||||  |||| || |  ::||||||||| |||||||  ||    :
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Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAY----WGQGTTVTVSS 116
              ||||:|||||||||| ||||:||| |||:||| :|||||| |:|     ||:|| |||||
Db         61 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGSYGMDVWGRGTMVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              ||||||||||||||||::||||: :||| |:|||:|| ||  :  :: |:||| | :||
Db        121 GGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
                ||  | |:|| |:|||||||| ::||||:: :| |||||||:|: ||||| |||||
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Db        181 LLIYKASSLASGAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
              : |||
Db        241 ILRAA 245


RESULT 15
US-09-138-091A-74
; Sequence 74, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia W.
;  APPLICANT:  Carter, Paul J.
;  APPLICANT:  Fendly, Brian M.
;  APPLICANT:  Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: 9491-013-27
;  CURRENT APPLICATION NUMBER: US/09/138,091A
;  CURRENT FILING DATE:  1998-08-21
;  PRIOR APPLICATION NUMBER: US 60/056,736
;  PRIOR FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: single chain antibody (scFv) fragments
US-09-138-091A-74

  Query Match             54.3%;  Score 881.5;  DB 4;  Length 245;
  Best Local Similarity   68.2%;  Pred. No. 2.9e-58;
  Matches  167;  Conservative   33;  Mismatches   40;  Indels    5;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||||:| :||||:||||||  |||| || |  ::|||||||| |||||| ||    :
Db          1 MAEVQLVQSGGGVVQPGGSLSLSCAVSGITLRTYGMHWVRQAPGKGLEWVAGISFDGRSE 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAY----WGQGTTVTVSS 116
              ||||:|||||||||| ||||:||| |||:||| :|||||  |:|    ||:|| |||||
Db         61 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGSYGMDVWGRGTMVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              ||||||||||||||||::||||: :||| |:|||:|| ||  :  :: |:||| | :||
Db        121 GGGGSGGGGSGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYHWLAWYQQKPGKAPK 180

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
              ||  | |:|| |:|||||||| ::|||||:: :| |||||||:|: ||||| |||||
Db        181 LLIYKASSLASGAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYSNYPLTFGGGTKLE 240

Qy        236 LKRAA 240
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Db        241 ILRAA 245


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Job time : 39 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:55:04 ; Search time 142 Seconds
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800.521 Million cell updates/sec

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Perfect score: 1622
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VVLTIISLIILIMLWQKKPR 316

Scoring table: BLOSUM62
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Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1202252

Minimum DB seq length: 0
Maximum DB seq length: 316

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	959	59.1	291	15	US-10-406-830-10	Sequence 10, Appl
2	943.5	58.2	288	9	US-09-818-247-22	Sequence 22, Appl
3	927	57.2	291	15	US-10-406-830-9	Sequence 9, Appli
4	926	57.1	287	15	US-10-406-830-5	Sequence 5, Appli
5	913	56.3	242	14	US-10-259-087A-20	Sequence 20, Appl
6	913	56.3	242	17	US-10-689-006-20	Sequence 20, Appl
7	906.5	55.9	237	10	US-09-880-748-2104	Sequence 2104, Ap
8	906.5	55.9	237	14	US-10-293-418-2104	Sequence 2104, Ap
9	903.5	55.7	237	10	US-09-880-748-2020	Sequence 2020, Ap
10	903.5	55.7	237	14	US-10-293-418-2020	Sequence 2020, Ap
11	900.5	55.5	237	10	US-09-880-748-2005	Sequence 2005, Ap
12	900.5	55.5	237	10	US-09-880-748-2114	Sequence 2114, Ap
13	900.5	55.5	237	14	US-10-293-418-2005	Sequence 2005, Ap
14	900.5	55.5	237	14	US-10-293-418-2114	Sequence 2114, Ap
15	899.5	55.5	237	10	US-09-880-748-2118	Sequence 2118, Ap
16	899.5	55.5	237	14	US-10-293-418-2118	Sequence 2118, Ap
17	898.5	55.4	237	10	US-09-880-748-2115	Sequence 2115, Ap
18	898.5	55.4	237	14	US-10-293-418-2115	Sequence 2115, Ap
19	897.5	55.3	237	10	US-09-880-748-2027	Sequence 2027, Ap
20	897.5	55.3	237	10	US-09-880-748-2111	Sequence 2111, Ap
21	897.5	55.3	237	14	US-10-293-418-2027	Sequence 2027, Ap
22	897.5	55.3	237	14	US-10-293-418-2111	Sequence 2111, Ap
23	897	55.3	256	15	US-10-239-656-61	Sequence 61, Appl
24	896.5	55.3	237	10	US-09-880-748-2003	Sequence 2003, Ap
25	896.5	55.3	237	10	US-09-880-748-2017	Sequence 2017, Ap
26	896.5	55.3	237	10	US-09-880-748-2019	Sequence 2019, Ap
27	896.5	55.3	237	10	US-09-880-748-2028	Sequence 2028, Ap
28	896.5	55.3	237	10	US-09-880-748-2110	Sequence 2110, Ap
29	896.5	55.3	237	14	US-10-293-418-2003	Sequence 2003, Ap
30	896.5	55.3	237	14	US-10-293-418-2017	Sequence 2017, Ap
31	896.5	55.3	237	14	US-10-293-418-2019	Sequence 2019, Ap
32	896.5	55.3	237	14	US-10-293-418-2028	Sequence 2028, Ap
33	896.5	55.3	237	14	US-10-293-418-2110	Sequence 2110, Ap
34	895.5	55.2	237	10	US-09-880-748-1906	Sequence 1906, Ap
35	895.5	55.2	237	14	US-10-293-418-1906	Sequence 1906, Ap
36	894.5	55.1	237	10	US-09-880-748-2040	Sequence 2040, Ap
37	894.5	55.1	237	14	US-10-293-418-2040	Sequence 2040, Ap
38	894	55.1	240	9	US-09-192-854-2	Sequence 2, Appli
39	894	55.1	240	9	US-09-968-561A-2	Sequence 2, Appli
40	894	55.1	240	10	US-09-968-744A-2	Sequence 2, Appli
41	894	55.1	240	11	US-09-968-561A-2	Sequence 2, Appli
42	894	55.1	240	17	US-10-744-774-1	Sequence 1, Appli
43	894	55.1	248	10	US-09-880-748-1421	Sequence 1421, Ap
44	894	55.1	248	14	US-10-293-418-1421	Sequence 1421, Ap
45	889.5	54.8	237	10	US-09-880-748-2043	Sequence 2043, Ap

ALIGNMENTS

RESULT 1
US-10-406-830-10
; Sequence 10, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
US-10-406-830-10

Query Match 59.1%; Score 959; DB 15; Length 291;
Best Local Similarity 70.1%; Pred. No. 2.5e-57;
Matches 185; Conservative 31; Mismatches 38; Indels 10; Gaps 2;

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Db        141 VTVSSGGGGSGGGGSGGGGSEIVLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKP 200

Qy        171 GTSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGA 230
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Db        201 GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQYNSYPWTFGQ 260

Qy        231 GTKLELKRAAAEQKLISEEDLNGA 254
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RESULT 2
US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
;  APPLICANT: Mostov, Keith E.
;  APPLICANT:  Chapin, Steven J.
;  APPLICANT:  Richman-Eisenstat, Janice
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,
;  TITLE OF INVENTION:  No. US20020102657A1-Stalk Region of pIgR and Methods of Use Ther
;  FILE REFERENCE: 18062E-000910US
;  CURRENT APPLICATION NUMBER: US/09/818,247
;  CURRENT FILING DATE:  2001-03-26
;  PRIOR APPLICATION NUMBER: WO PCT/US01/09699
;  PRIOR FILING DATE: 2001-03-26
;  PRIOR APPLICATION NUMBER: US 60/192,197
;  PRIOR FILING DATE: 2000-03-27
;  PRIOR APPLICATION NUMBER: US 60/192,198
;  PRIOR FILING DATE: 2000-03-27
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial
;   OTHER INFORMATION: Sequence:Pelb/4AF/myc/6HIS
US-09-818-247-22

  Query Match           58.2%;  Score 943.5;  DB 9;  Length 288;
  Best Local Similarity 69.3%;  Pred. No. 2.8e-56;
  Matches  181;  Conservative   32;  Mismatches   41;  Indels    7;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
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Qy        115 SSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTS 173
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Qy        174 PKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTK 233
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Qy        234 LELKRAAAEQKLISEEDLNGA 254
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Db        261 VDIKRAAAEQKLISEEDLNGA 281


RESULT 3
US-10-406-830-9
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; Sequence 9, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
;  APPLICANT: ADAMS, GREGORY P.
;  APPLICANT:  HORAK, EVA M.
;  APPLICANT:  WEINER, LOUIS M.
;  APPLICANT:  JAMES, MARKS D.
;  TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 407T-000410US
;  CURRENT APPLICATION NUMBER: US/10/406,830
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/370,276
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 291
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic antibody.
US-10-406-830-9

  Query Match           57.2%;  Score 927;  DB 15;  Length 291;
  Best Local Similarity 67.4%;  Pred. No. 3.7e-55;
  Matches  178;  Conservative   36;  Mismatches   40;  Indels   10;  Gaps    2;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:| : |||||||||| :|||||||||||: | |||||| ||||:: ||    :
Db         21 MAQVQLLQFGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWLSAISGSGGST 80

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD---------YGAYWGQGTT 111
              ||||:|||||||||| ||||:||| |||:||| :||||:         |   ||:||
Db         81 YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGYSSNWNNWYFDLWGRGTL 140

Qy        112 VTVSSGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKS 170
              |||||||||||||||||||: :|||| :||| |:|||:|| || |:  |:||:|||
Db        141 VTVSSGGGGSGGGGSGGGGSDVVMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKP 200

Qy        171 GTSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGA 230
              | :|:  ||  |:| ||||:||||||||| ::|||||:: :| |||| ||: : | |||
Db        201 GKAPELLIYAASRLQSGVPSRFSGSGSGTEFTLTISSLQPDDFATYYGQQYYNYPWTFGR 260

Qy        231 GTKLELKRAAAEQKLISEEDLNGA 254
              |||:|:||||||||||||||||||
Db        261 GTKVEIKRAAAEQKLISEEDLNGA 284


RESULT 4
US-10-406-830-5
; Sequence 5, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
;  APPLICANT: ADAMS, GREGORY P.
;  APPLICANT:  HORAK, EVA M.
;  APPLICANT:  WEINER, LOUIS M.
;  APPLICANT:  JAMES, MARKS D.
;  TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 407T-000410US
;  CURRENT APPLICATION NUMBER: US/10/406,830
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/370,276
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic antibody.
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US-10-406-830-5

Query Match 57.1%; Score 926; DB 15; Length 287;
Best Local Similarity 69.6%; Pred. No. 4.3e-55;
Matches 181; Conservative 32; Mismatches 41; Indels 6; Gaps 3;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|:| |||||:|||| | :|||||||||||| : :||||||| |||||:| ||   :
Db         21 MAQVQLVESGGGVVQPGRSLRLSCAASGFTFSDYYIHWVRQAPGKGLEWMAVISYDGNNK 80

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD-YG----AYWGQGTTVTVS 115
              ||| :|| |||||||| |||: ||| |||:||| :|||||| ||     |||||| ||||
Db         81 YYAASVKDRFTISRDNSKNTVSLQMNSLRAEDTAVYYCARDLYGDYALDYWGQGTLVTVS 140

Qy        116 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSP 174
              |||||||||||||||||::|||| :||| |:|||:|| || |:  :: |:||| | :|
Db        141 SGGGGSGGGGSGGGGSDIQMTQSPSTLSASLGDRVTITCRASQSIGSWLAWYQQKPGKAP 200

Qy        175 KRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKL 234
              |  ||  | | ||||:||:|||||| ::|||| :: || ||||||: || ||||| |||:
Db        201 KLLIYKASTLESGVPSRFTGSGSGTEFTLTISGLQPEDFATYYCQKLSSYPLTFGGGTKV 260

Qy        235 ELKRAAAEQKLISEEDLNGA 254
              |:||||||||||||||||||
Db        261 EIKRAAAEQKLISEEDLNGA 280
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RESULT 5
US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Qu, Shimian
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259,087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

Query Match 56.3%; Score 913; DB 14; Length 242;
Best Local Similarity 71.1%; Pred. No. 2.7e-54;
Matches 172; Conservative 30; Mismatches 36; Indels 4; Gaps 2;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:||  ||:|| | |:|| |||:||:|: ||||:| | :||||: ||:  :
Db          1 MAQVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGT 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR--DYGA--YWGQGTTVTVSS 116
                | :  ||:  :: |   :| :::::|| |||: :|||||  :|||  ||||||||||||
Db         61 KYNEKFKGKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYGALDYWGQGTTVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKR 176
              |||||||||||||||||||||| ||||||||:||:|||||||| ||:||||| |||||
Db        121 GGGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKP 180

Qy        177 WIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 236
              ||| || |:|||| |||||||||||||||||||||||||||||||| ||||| |||||:
Db        181 WIYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSYPLTFGGGTKLEI 240

Qy        237 KR 238
              ||
Db        241 KR 242
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RESULT 6
US-10-689-006-20
; Sequence 20, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20

Query Match 56.3%; Score 913; DB 17; Length 242;
Best Local Similarity 71.1%; Pred. No. 2.7e-54;
Matches 172; Conservative 30; Mismatches 36; Indels 4; Gaps 2;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:||  ||:|| | |:|| |||:||:|: ||||:| | :||||: ||:  :
Db          1 MAQVKLQQSGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGT 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR--DYGA--YWGQGTTVTVSS 116
                | :  ||:  :: |   :| :::::|| |||: :|||||  :|||  ||||||||||||
Db         61 KYNEKFKGKAALTSDKSSSTAYMELSSLTSEDSAVYYCARFGNYGALDYWGQGTTVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKR 176
              |||||||||||||||||||||| ||||||||:||:|||||||| ||:||||| |||||
Db        121 GGGGSGGGGSGGGGSDIELTQSPTIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKP 180

Qy        177 WIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 236
              ||| || |:|||| |||||||||||||||||||||||||||||||| ||||| |||||:
Db        181 WIYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSYPLTFGGGTKLEI 240

Qy        237 KR 238
              ||
Db        241 KR 242
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RESULT 7
US-09-880-748-2104
; Sequence 2104, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499

```
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2104
;    LENGTH: 237
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-2104

  Query Match            55.9%;  Score 906.5;  DB 10;  Length 237;
  Best Local Similarity  72.6%;  Pred. No. 7.4e-54;
  Matches  172;  Conservative   28;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||||||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTTVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||||| :|||| :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 8
US-10-293-418-2104
; Sequence 2104, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2104
;    LENGTH: 237
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-293-418-2104

  Query Match            55.9%;  Score 906.5;  DB 14;  Length 237;
  Best Local Similarity  72.6%;  Pred. No. 7.4e-54;
  Matches  172;  Conservative   28;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||||||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTTVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||||| :|||| :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 9
US-09-880-748-2020
; Sequence 2020, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2020
;    LENGTH: 237
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-880-748-2020

  Query Match            55.7%;  Score 903.5;  DB 10;  Length 237;
  Best Local Similarity  72.6%;  Pred. No. 1.2e-53;
  Matches  172;  Conservative   27;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              ||:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTLVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||||| :|||| :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 10
US-10-293-418-2020
; Sequence 2020, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
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;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2020
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-2020

  Query Match            55.7%;  Score 903.5;  DB 14;  Length 237;
  Best Local Similarity  72.6%;  Pred. No. 1.2e-53;
  Matches  172;  Conservative   27;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              ||:| :||||||||||| :|||||||||||: |:|||||| |||||:|||| |||||
Db          1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:|||||||||| ||:|:||| |||:||| :|||||   |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTLVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||: :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:|||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 11
US-09-880-748-2005
; Sequence 2005, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2005
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2005

  Query Match            55.5%;  Score 900.5;  DB 10;  Length 237;
  Best Local Similarity  72.2%;  Pred. No. 1.9e-53;
  Matches  171;  Conservative   28;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| |||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:|||||||||| ||:|:||| |||:||| :|||||   |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTMVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||| :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:|||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 12
US-09-880-748-2114
; Sequence 2114, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2114
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2114

  Query Match            55.5%;  Score 900.5;  DB 10;  Length 237;
  Best Local Similarity  72.2%;  Pred. No. 1.9e-53;
  Matches  171;  Conservative   28;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| |||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:|||||||||| ||:|:||| |||:||| :|||||   |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTMVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||| :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:|||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 13
US-10-293-418-2005
; Sequence 2005, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
```

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;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2005
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-2005

  Query Match             55.5%;  Score 900.5;  DB 14;  Length 237;
  Best Local Similarity   72.2%;  Pred. No. 1.9e-53;
  Matches  171;  Conservative   28;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTLVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||: :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 14
US-10-293-418-2114
; Sequence 2114, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2114
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-2114

  Query Match             55.5%;  Score 900.5;  DB 14;  Length 237;
  Best Local Similarity   72.2%;  Pred. No. 1.9e-53;
  Matches  171;  Conservative   28;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTMVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||: :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLAWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              | | ||||:||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237


RESULT 15
US-09-880-748-2118
; Sequence 2118, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2118
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-2118

  Query Match             55.5%;  Score 899.5;  DB 10;  Length 237;
  Best Local Similarity   72.2%;  Pred. No. 2.2e-53;
  Matches  171;  Conservative   28;  Mismatches   37;  Indels    1;  Gaps    1;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| :||||||||||| :|||||||||||: |:|||||| ||||||:|||| |||||
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSG 122
              ||:||||||||||| ||:|:||| |||:||| :|||||    |||||| ||||||||||
Db         61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTLVTVSSGGGGSG 120

Qy        123 GGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIYDT 181
              |||||||||| :|||: :||| |:|||:|| ||  :  :: |:||| | :||  ||
Db        121 GGGSGGGGSDIVMTQSPSTLSASVGDRVTITCRASQGISSWLVWYQQKPGRAPKVLIYKA 180

Qy        182 SKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
```

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                 | | ||||:|||||||||| ::|||||:: || |||||||  | | ||| |||||:||
Db        181 STLESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPWTFGQGTKLEIKR 237

Search completed: December 30, 2004, 16:07:11
Job time : 143 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:46:06 ; Search time 40 Seconds
(without alignments)
760.112 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VVLTIISLIILIMLWQKKPR 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 164529

Minimum DB seq length: 0
Maximum DB seq length: 316

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	892.5	55.0	268	2	A56446	Ig heavy chain V r
2	718.5	44.3	249	2	S41374	single chain Fv an
3	626.5	38.6	233	2	JC5322	p53 specific singl
4	555.5	34.2	213	2	S68213	Ig heavy chain (Ma
5	535	33.0	136	1	G1MS21	Ig heavy chain pre
6	522.5	32.2	121	2	B34871	Ig heavy chain V r
7	516	31.8	130	1	JL0079	Ig kappa chain pre
8	514	31.7	235	2	S25058	Ig kappa chain - m
9	511	31.5	107	2	A30562	Ig kappa chain V r
10	508	31.3	103	2	S29591	Ig kappa chain V r
11	508	31.3	104	2	B49049	Ig kappa chain V r
12	506	31.2	106	2	PS0071	Ig kappa chain V r
13	506	31.2	107	2	B30562	Ig kappa chain V r
14	501	30.9	107	2	S11118	Ig kappa chain V r
15	498	30.7	107	2	S11119	Ig kappa chain V r
16	498	30.7	107	2	PC4405	Ig kappa chain V r
17	490	30.2	107	2	S11121	Ig kappa chain V r
18	488	30.1	107	2	PT0406	Ig kappa chain V r
19	484.5	29.9	143	2	S23624	Ig heavy chain V r
20	483	29.8	107	2	S11117	Ig kappa chain V r
21	482	29.7	120	2	S12953	Ig heavy chain V r
22	481.5	29.7	108	2	G30560	Ig kappa chain V r
23	480	29.6	94	2	D25913	Ig heavy chain V r
24	479	29.5	100	2	S29590	Ig kappa chain V r
25	479	29.5	107	2	S11112	Ig kappa chain V r
26	478	29.5	108	2	PH1015	Ig heavy chain V r
27	476	29.3	107	2	PD0011	Ig kappa chain V r
28	473	29.2	97	2	PH1084	Ig light chain V r
29	473	29.2	114	2	S46392	Ig heavy chain V r
30	471.5	29.1	123	2	S26794	Ig heavy chain V r
31	471.5	29.1	125	2	S30531	Ig heavy chain V r
32	471	29.0	114	2	S46391	Ig heavy chain V r
33	470	29.0	110	2	PH1014	Ig heavy chain V r
34	470	29.0	114	2	S46390	Ig heavy chain V r
35	469	28.9	107	2	S11113	Ig kappa chain V r
36	468	28.9	97	2	S26341	Ig light chain V r
37	467	28.8	106	2	G27887	Ig kappa chain V r
38	466	28.7	140	2	S70442	Ig heavy chain pre
39	463	28.5	106	2	B54378	Ig light chain V r
40	462	28.5	104	2	JC6076	anti-D-dimer monoc
41	461.5	28.5	108	2	S38720	Ig light chain V r
42	461.5	28.5	120	2	S55536	Ig heavy chain V r
43	461	28.4	130	2	S04573	Ig kappa chain pre
44	460.5	28.4	120	2	S66536	Ig light chain V r
45	459.5	28.3	106	2	S11114	Ig kappa chain V r

ALIGNMENTS

RESULT 1
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 892.5; DB 2; Length 268;
Best Local Similarity 65.9%; Pred. No. 1.2e-52;
Matches 176; Conservative 26; Mismatches 52; Indels 13; Gaps 2;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:|||||||  ||:|| | ||||  |||      ||||:| ||:||||:  |:  :
Db          1 MAQVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGIT 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCA----RDYGAYWGQGTTVTVSS 116
                 |    :|: ||: |   || :||::|| |||| :||||      |  ||||||||||||
Db         61 KYDPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCASYYLTRYENYWGQGTTVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKR 176
              |||||||| |||||||||||||||||| ||:|||:| ||||| :: |:||||  |||
Db        121 GGGGSGGGDSGGGGSDIELTQSPAIMSASLGEKVTMSCRASSSVNFIYWYQQKSDASPKL 180

Qy        177 WIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 236
              |:| || |  |||||||||||| |||||||||| ||||||||||::|:| |||:|||||:
Db        181 WVYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCQQFTSSPFTFGSGTKLEI 240

Qy        237 KRA---------AAEQKLISEEDLNGA 254
              ||:         ||||||||||||||
Db        241 KRSAAHHHHHHGAAEQKLISEEDLNGA 267
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RESULT 2
S41374
single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antibod
A;Reference number: S41374

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A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480

  Query Match             44.3%;  Score 718.5;  DB 2;  Length 249;
  Best Local Similarity   57.8%;  Pred. No. 4.7e-41;
  Matches  144;  Conservative   31;  Mismatches   63;  Indels   11;  Gaps    3;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:||:||  ||:|| | |||| |||| |    :|||:| |||||||:| |:  |  : |
Db          1 QVQLQQSGAELVRPGASVKLSCTASGFNFKDDYIHWVKQRPEKGLEWIARIAPASGNVKY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD---YGA--YWGQGTTVTVSSG 117
                : : ||: |   || :| ::|| |||| :|||||    | :  |||||:||||||
Db         61 VPRFQDKATITADTSSNTAYLLLSSLTSEDTAVYYCARRDTLYTSLGYWGQGSTVTVSSR 120

Qy        118 GGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV------RYMNWFQQKSG 171
              |||||||||||||||||||||  :   ||| |:::| :| |:       |: || |: |
Db        121 GGGSGGGGSGGGGSDIELTQSPPSVVVIPGESVSISCRSSKSLLYSDGDSYLFWFLQRPG 180

Qy        172 TSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAG 231
              ||:  ||  | |:|||| ||||||||||::| || :||||   ||| |    |||||||
Db        181 QSPQLLIYRMSNLASGVPDRFSGSGSGTSFTLRISRVEAEDVGVYYCMQHREYPLTFGAG 240

Qy        232 TKLELKRAA 240
              |||||||||
Db        241 TKLELKRAA 249


RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C;Accession: JC5322
R;Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores

  Query Match             38.6%;  Score 626.5;  DB 2;  Length 233;
  Best Local Similarity   55.3%;  Pred. No. 6.1e-35;
  Matches  131;  Conservative   29;  Mismatches   66;  Indels   11;  Gaps    5;

Qy          7 QESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYI--SSGSSTIYYAD 64
              ||||  ||: | | ||||  |||  : : ||||:: ||:||||:  |   :| : :  :
Db          1 QESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSS 60

Qy         65 TVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTTVTVSSGGGGSGGG 124
                ||   |:: |   || :||::|| |||| :|||      ||||||||||||||||||
Db         61 GVKA--TMTADTSSNTAYLQLSSLTSEDTAVYYCNAGMD-YWGQGTTVTVSSGGGGSGGR 117

Qy        125 GSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-----RYMNWFQQKSGTSPKRWIY 179
              |||||||||||||| :: | |:| |::| || ||      ||:| ||| |  |:  ||
Db        118 ASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPPRLLIY 177

Qy        180 DTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEL 236
              | | |||||||||||||| ::| |  :| |||||||||      : | |||||:
Db        178 LVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHIRELTRSEG-GTKLEI 233


RESULT 4
S68213
Ig heavy chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: S68213
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin H
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68213
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-213 <TAK>
A;Cross-references: UNIPROT:Q91Z05; EMBL:D29667
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;137-201/Domain: immunoglobulin homology <IMM>

  Query Match             34.2%;  Score 555.5;  DB 2;  Length 213;
  Best Local Similarity   53.9%;  Pred. No. 3.1e-30;
  Matches  124;  Conservative   17;  Mismatches   50;  Indels   39;  Gaps    5;

Qy          4 VKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYA 63
              |:| |||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db          2 VQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSSIYYA 61

Qy         64 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDY---GAYWGQGTTVTVSSGGGG 120
              |||||||||||||||||||||||||||||| |||||| :     |||||||:||||
Db         62 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARSWLLPFDYWGQGTTLTVSSA--- 118

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYD 180
                          | |::   :||   |   | :       :| :    :     ::
Db        119 -------------KTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT-----WN 159

Qy        181 TSKLSSGV---PARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLT 227
              :  ||| |   ||          | |:|: |           | |  :|
Db        160 SGSLSSSVHTFPALLQSGLYTMSSSVTVPS-----------STWPSQTVT 198


RESULT 5
G1MS21
Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: E90809; A93184; A02066
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: soma
A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: E90809
A;Molecule type: mRNA
A;Residues: 1-136 <BOT>
A;Cross-references: UNIPROT:P01783; GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055
R;Adetugbo, K.; Milstein, C.; Secher, D.S.
Nature 265, 299-304, 1977
A;Title: Molecular analysis of spontaneous somatic mutants.
A;Reference number: A93184; MUID:77100368; PMID:401950
A;Contents: myeloma protein MOPC 21
A;Accession: A93184
A;Molecule type: protein
A;Residues: 17-74,'D',76-77,'H',79-88,'ND',91-114,'H',116-119,'W',121-136 <ADE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
F;31-114/Domain: immunoglobulin homology <IMM>
F;115-119/Region: D segment
F;120-136/Region: J segment (JH4)
F;38-112/Disulfide bonds: #status experimental

  Query Match             33.0%;  Score 535;  DB 1;  Length 136;
  Best Local Similarity   87.5%;  Pred. No. 4.4e-29;
  Matches  105;  Conservative    5;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| |||||||||||||||||||||||||||||||||||||||||||||||||||::|
Db         17 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHY 76
```

```
Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR----DYGA--YWGQGTTVTVSS 116
              ||||||||||||||||||||||||||||||| ||||||     | |  ||||||:||||
Db         77 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYYAMDYWGQGTSVTVSS 136
```

RESULT 6
B34871
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Feb-1991 #sequence_revision 13-Sep-1991 #text_change 16-Aug-1996
C;Accession: B34871
R;Chaudhary, V.K.; Batra, J.K.; Gallo, M.G.; Willingham, M.C.; FitzGerald, D.J.; Pastan,
Proc. Natl. Acad. Sci. U.S.A. 87, 1066-1070, 1990
A;Title: A rapid method of cloning functional variable-region antibody genes in Escheric
A;Reference number: A34871; MUID:90138938; PMID:2105495
A;Accession: B34871
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <CHA>
A;Cross-references: GB:M34000
A;Note: the authors translated the codon GTG for residue 119 as Gly
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match 32.2%; Score 522.5; DB 2; Length 121;
  Best Local Similarity 83.5%; Pred. No. 2.7e-28;
  Matches 101; Conservative 7; Mismatches 6; Indels 7; Gaps 2;

```
Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||:||||||||||||||||||||||||||||||| | :||||
Db          1 DVQLVESGGGLVQPGGSRQLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISRGGNTIYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD--YG-----AYWGQGTTVTVS 115
              |:|||||||||||||||||||||||:|| ||||||   ||      |||||||:|||
Db         61 ANTVKGRFTISRDNPKNTLFLQMTSLRSDDTAMYYCARSHYYGYFYAMDYWGQGTTLTVS 120

Qy        116 S 116
              |
Db        121 S 121
```

RESULT 7
JL0079
Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: JL0079; A49044; B49044
R;Kaartinen, M.; Rocca-Serra, J.; Maekelae, O.
Mol. Immunol. 25, 859-865, 1988
A;Title: Combinatorial association of V genes: one VH gene codes for three non-cross-rea
A;Reference number: JL0076; MUID:89096973; PMID:3211160
A;Accession: JL0079
A;Molecule type: mRNA
A;Residues: 1-130 <KAA>
A;Cross-references: GB:M27792; NID:g197159
A;Experimental source: mRNA clones for anti-phenyloxazolone antibody 6F6
A;Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A;Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R;Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A;Title: Non-random features of the repertoire expressed by the members of one V kappa g
A;Reference number: A49044; MUID:92289826; PMID:1601044
A;Accession: A49044
A;Molecule type: DNA
A;Residues: 1-25 <MIL>
A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; PID:g250217
A;Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIP:106809)
A;Accession: B49044
A;Molecule type: DNA
A;Residues: 114-116 <MIL2>
A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; PID:g250218
A;Experimental source: BALB/c germ-line
A;Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit
A;Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBIP:106822)
C;Genetics:
A;Gene: V(kappa)Ox1
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F;38-111/Domain: immunoglobulin homology <IMM>
F;45-109/Disulfide bonds: #status predicted

  Query Match 31.8%; Score 516; DB 1; Length 130;
  Best Local Similarity 92.5%; Pred. No. 7.8e-28;
  Matches 99; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:||||||||||| ||:|:|||||||||||||||||:|||||||
Db         24 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 83

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRA 239
              |||||| |||||||||||||||||||||||||||||||||||| |||
Db         84 SGSGSGXSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLEXKRA 130
```

RESULT 8
S25058
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific n
A;Reference number: S25057
A;Accession: S25058
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <FIS>
A;Cross-references: EMBL:X67211; NID:g54828; PIDN:CAA47650.1; PID:g54829
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-111/Domain: immunoglobulin homology <IMM>

  Query Match 31.7%; Score 514; DB 2; Length 235;
  Best Local Similarity 91.7%; Pred. No. 2e-27;
  Matches 100; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```
Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:||||||||||  | |:|||||||||||||||||:|||| ||
Db         24 IVLTQSPAIMSASPGEKVTMTCSASSSVSKMQWYQQKSGTSPKRWIYDTSKLASGVPGRF 83

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
              |||||||||||||||||||||||||||||||||||||||||||||||| |
Db         84 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRADA 132
```

RESULT 9
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: A30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: A30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             31.5%;  Score 511;  DB 2;  Length 107;
  Best Local Similarity   91.5%;  Pred. No. 1.4e-27;
  Matches   97;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||||:|||||||||| ||:|:||||||||||||||||:|||||||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              |||||||||||||||||||||||||||||||| ||| |||||:||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIKR 107


RESULT 10
S29591
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S29591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <KAV>
A;Cross-references: EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:g52228
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-88/Domain: immunoglobulin homology <IMM>

  Query Match             31.3%;  Score 508;  DB 2;  Length 103;
  Best Local Similarity   94.2%;  Pred. No. 2.1e-27;
  Matches   97;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:|||||||||| ||:|:||||||||||||||||:|||||||
Db          1 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 60

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 103


RESULT 11
B49049
Ig kappa chain V region (anti-idiotypic) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B49049
R;Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
Eur. J. Immunol. 22, 2893-2899, 1992
A;Title: Molecular analysis of anti-idiotypic monoclonal antibodies in the HLA-DR antige
A;Reference number: A49049; MUID:93049629; PMID:1425914
A;Accession: B49049
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-104 <ARM>
A;Experimental source: BALB/c
A;Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             31.3%;  Score 508;  DB 2;  Length 104;
  Best Local Similarity   94.2%;  Pred. No. 2.1e-27;
  Matches   97;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:|||||||||| ||:|:||||||||||||||||:|||||||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLTSGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
              |||||||||||||||||||||||||||||||||||||||||||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 104


RESULT 12
PS0071
Ig kappa chain V region (38C13.V8) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: PS0071
R;Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangemer
A;Reference number: A92781; MUID:89310348; PMID:2501443
A;Accession: PS0071
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <LEV>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             31.2%;  Score 506;  DB 2;  Length 106;
  Best Local Similarity   92.4%;  Pred. No. 2.9e-27;
  Matches   97;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:|||||||||| ||:|:||||||||||||||||:|||||||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELK 237
              |||||||||||||||||||||||||||||||||||:|||| ||||||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPVTFGAPTKLELK 106


RESULT 13
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L
J. Immunol. 142, 888-893, 1989
A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir
A;Reference number: A30562; MUID:89110066; PMID:2464031
A;Accession: B30562
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <SIK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             31.2%;  Score 506;  DB 2;  Length 107;
  Best Local Similarity   89.6%;  Pred. No. 3e-27;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:|||||||||| ||:|:||||||||||:|||||:|||| ||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWVYDTSKLASGVPTRF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              |||||||||||||||||||||||||||||||| ||| |||||:||
Db         62 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIKR 107


RESULT 14
S11118
Ig kappa chain V region (clone NQ5-61.1.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
```

```
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
C;Accession: S11118
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <KAA>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             30.9%;  Score 501;  DB 2;  Length 107;
  Best Local Similarity   91.5%;  Pred. No. 6.4e-27;
  Matches   97;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||:|||||||||| ||:|:||||||||||||||||| |||||||
Db          2 IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLDSGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||||||||||||| |||||||||||||||||||||||| | |
Db         62 SGSGSGTSYSLTISSMFAEDAATYYCQQWSSNPLTFGAGTKLXLXR 107


RESULT 15
S11119
Ig kappa chain V region (clone NQ6-8.3.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change 21-Jan-2000
C;Accession: S11119
R;Kaartinen, M.; Griffiths, G.M.; Markham, A.F.; Milstein, C.
Nature 304, 320-324, 1983
A;Title: mRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone
A;Reference number: S07331; MUID:83271467; PMID:6877353
A;Accession: S11119
A;Molecule type: mRNA
A;Residues: 1-107 <NAT>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             30.7%;  Score 498;  DB 2;  Length 107;
  Best Local Similarity   89.6%;  Pred. No. 1e-26;
  Matches   95;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | ||||| ||| |||||:|||||||||||| ||:|:|||||||||||||||||:|||||||
Db          2 IVLTQSPXIMSXSPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              || | |||||||||||| |||||||||||||||||||||||||||
Db         62 SGXGXGTSYSLTISSMFAEDAATYYCQQWSSNPLTFGAGTKLELKR 107


Search completed: December 30, 2004, 15:55:36
Job time : 42 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 30, 2004, 15:38:05 ; Search time 188 Seconds
(without alignments)
967.119 Million cell updates/sec

Title: US-09-403-882A-2
Perfect score: 1622
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VVLTIISLIILIMLWQKKPR 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1144693

Minimum DB seq length: 0
Maximum DB seq length: 316

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	853.5	52.6	298	2	Q9QYF0	Q9qyf0 synthetic c
2	850	52.4	255	2	Q6KB05	Q6kb05 mus musculu
3	850	52.4	255	2	CAG34081	Cag34081 mus muscu
4	695	42.8	241	2	Q921A6	Q921a6 mus musculu
5	658	40.6	243	2	Q7TQM2	Q7tqm2 mus musculu
6	608.5	37.5	218	2	Q925S1	Q925s1 mus musculu
7	535	33.0	136	1	HV16_MOUSE	P01783 mus musculu
8	507	31.3	107	1	KV6F_MOUSE	P04940 mus musculu
9	506	31.2	107	1	KV6H_MOUSE	P04942 mus musculu
10	502	30.9	107	1	KV6I_MOUSE	P04943 mus musculu
11	500	30.8	107	1	KV6G_MOUSE	P04941 mus musculu
12	498	30.7	112	2	Q8K1F0	Q8k1f0 mus musculu
13	494	30.5	107	1	KV6J_MOUSE	P04944 mus musculu
14	491	30.3	235	2	Q91W12	Q91w12 mus musculu
15	483	29.8	134	2	Q8VDD0	Q8vdd0 mus musculu
16	480	29.6	112	2	Q8K1F2	Q8k1f2 mus musculu
17	462.5	28.5	113	2	Q9UL90	Q9ul90 homo sapien
18	461	28.4	112	2	Q8K1F3	Q8k1f3 mus musculu
19	458	28.2	111	2	AAR10981	Aar10981 mus muscu
20	458	28.2	111	2	AAR10982	Aar10982 mus muscu
21	458	28.2	114	2	Q8K1F1	Q8k1f1 mus musculu
22	457	28.2	108	2	AAR11048	Aar11048 mus muscu
23	453	27.9	92	2	AAR11066	Aar11066 mus muscu
24	452.5	27.9	119	2	Q920E7	Q920e7 mus musculu
25	450.5	27.8	128	2	BAD00406	Bad00406 camelus d
26	447	27.6	110	2	AAR10999	Aar10999 mus muscu
27	447	27.6	121	2	BAD00469	Bad00469 camelus d
28	446.5	27.5	119	2	AAL35865	Aal35865 lama glam
29	446	27.5	107	1	KV6C_MOUSE	P01677 mus musculu
30	446	27.5	124	2	BAD00233	Bad00233 camelus d
31	445.5	27.5	117	2	AAL35877	Aal35877 lama glam
32	445	27.4	118	2	Q9UL91	Q9ul91 homo sapien
33	443	27.3	119	2	BAD00422	Bad00422 camelus d
34	442.5	27.3	126	2	BAD00440	Bad00440 camelus d
35	441	27.2	107	1	KV6B_MOUSE	P01676 mus musculu
36	440.5	27.2	116	2	Q9UL93	Q9ul93 homo sapien
37	440	27.1	107	1	KV6D_MOUSE	P01678 mus musculu
38	439	27.1	119	2	BAD00492	Bad00492 camelus d
39	438.5	27.0	123	2	BAD00234	Bad00234 camelus d
40	438.5	27.0	124	2	BAD00534	Bad00534 camelus d
41	438.5	27.0	128	2	BAD00444	Bad00444 camelus d
42	438.5	27.0	131	2	Q811C3	Q811c3 mus musculu
43	438	27.0	118	2	AAL35882	Aal35882 lama glam
44	437.5	27.0	126	2	BAD00510	Bad00510 camelus d
45	437	26.9	106	2	Q9U410	Q9u410 schistosoma

ALIGNMENTS

RESULT 1
Q9QYF0
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CN 8 single chain antibody.
GN Name=CN 8 scFv;
OS synthetic construct.
OC artificial sequences.
OX NCBI_TaxID=32630;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A7O.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.6%; Score 853.5; DB 2; Length 298;
Best Local Similarity 66.3%; Pred. No. 3.2e-54;
Matches 163; Conservative 32; Mismatches 46; Indels 5; Gaps 2;

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Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:||||||:|||| |||||||| || : | |||||| |||||:  |:  ||||
Db         38 MAQVKLQQSGGGLVKPGGSLKLSCAASGSDFSRYWMSWVRQAPGKGLEWIGEINPDSSTI 97

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR----DYGAYWGQGTTVTVSS 116
                |  ::| :| ||||| ||||:|||: :||||| :|||||     : ||||||||||||
Db         98 NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYYGHSAYWGQGTTVTVSS 157

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPK 175
              |||||||||||||||||||||||| :||| || ||:|| || ::  |: |:||| | ||:
Db        158 GGGGSGGGGSGGGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQ 217

Qy        176 RWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE 235
              :|:   |: |||:|||||||| ||| |:|:: ||  :|||| : : | ||| |||||
Db        218 LLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLE 277

Qy        236 LKRAAA 241
              :|||||
Db        278 IKRAAA 283
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RESULT 2
Q6KB05
ID   Q6KB05      PRELIMINARY;      PRT;   255 AA.
AC   Q6KB05;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ScFv B8E5 protein (Fragment).
GN   Name=scFv B8E5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/c;
RA   Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA   Briand J.P., Hoebeke J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ746180; CAG34081.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   255 AA;  27445 MW;  B68BD38395DF713B CRC64;

  Query Match             52.4%;  Score 850;  DB 2;  Length 255;
  Best Local Similarity   67.1%;  Pred. No. 4.8e-54;
  Matches  167;  Conservative   29;  Mismatches   39;  Indels   14;  Gaps    4;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:||:||| ||:|||| |:||||||||||:|| |||| |:| ||||| |:|| |  ||
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR--DY---GA--YWGQGTTVTVS 115
               |:||||||||||| ||||:|||:||:|||| ||||||  :|   ||  |||||||:|||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHINYRYDGAFDYWGQGTTLTVS 120

Qy        116 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-------RYMNWFQQ 168
              |||||||||||||||| : |||: :| | ||:| |:| :| |:         |: |:||
Db        121 SGGGGSGGGGSGGGGSDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQ 180

Qy        169 KSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTF 228
              | | |||  ||  |   |||| ||:|||||| ::|||||::||| | ||||   | ||||
Db        181 KPGQSPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTF 240

Qy        229 GAGTKLELK 237
              |||||||:|
Db        241 GAGTKLEIK 249


RESULT 3
CAG34081
ID   CAG34081    PRELIMINARY;      PRT;   255 AA.
AC   CAG34081;
DT   01-JUN-2004 (TrEMBLrel. 27, Created)
DT   01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT   01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE   ScFv B8E5 protein (Fragment).
GN   SCFV B8E5.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb/c;
RA   Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA   Briand J.P., Hoebeke J.;
RT   "Modulation of the M2 muscarinic receptor activity with monoclonal
RT   anti-M2 receptor antibody fragments.";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ746180; CAG34081.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   255 AA;  27445 MW;  B68BD38395DF713B CRC64;

  Query Match             52.4%;  Score 850;  DB 2;  Length 255;
  Best Local Similarity   67.1%;  Pred. No. 4.8e-54;
  Matches  167;  Conservative   29;  Mismatches   39;  Indels   14;  Gaps    4;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:||:||| ||:|||| |:||||||||||:|| |||| |:| ||||| |:|| |  ||
Db          1 QVQLQQSGGDLVKPGGSLKVSCAASGFTFSSYGMSWVRQTPDKRLEWVATITSGGSYTYY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR--DY---GA--YWGQGTTVTVS 115
               |:||||||||||| ||||:|||:||:|||| ||||||  :|   ||  |||||||:|||
Db         61 PDSVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCARHINYRYDGAFDYWGQGTTLTVS 120

Qy        116 SGGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-------RYMNWFQQ 168
              |||||||||||||||| : |||: :| | ||:| |:| :| |:         |: |:||
Db        121 SGGGGSGGGGSGGGGSDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAWYQQ 180

Qy        169 KSGTSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTF 228
              | | |||  ||  |   |||| ||:|||||| ::|||||::||| | ||||   | ||||
Db        181 KPGQSPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTF 240

Qy        229 GAGTKLELK 237
              |||||||:|
Db        241 GAGTKLEIK 249


RESULT 4
Q921A6
ID   Q921A6      PRELIMINARY;      PRT;   241 AA.
AC   Q921A6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-CEA 79 single chain Fv (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98170165; PubMed=9509426;
RA   Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA   Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT   "Cloning and characterization of cDNAs encoding VH and VL of a
RT   monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT   generation of a single-chain Fv molecule (scFv).";
RL   Mol. Cells 7:816-819(1997).
DR   EMBL; U88067; AAB48044.1; -.
DR   PIR; S19965; S19965.
DR   PIR; S19967; S19967.
DR   PIR; S19968; S19968.
DR   PIR; S26325; S26325.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1       1
FT   NON_TER     241     241
SQ   SEQUENCE   241 AA;  26086 MW;  0276887248E9C771 CRC64;

  Query Match             42.8%;  Score 695;  DB 2;  Length 241;
  Best Local Similarity   55.7%;  Pred. No. 9.3e-43;
  Matches  137;  Conservative   40;  Mismatches   55;  Indels   14;  Gaps    5;
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Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :||||:||  | :|| : |:|| |||:||: :||:||:||| |||:|: :|:: :    |
Db          1 QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARD----YGAYWGQGTTVTVSSGG 118
              ||  |||| | :   :| :||: :|::|||  |:|||     |  |||||||||||||
Db         61 ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARKDLLRYFDYWGQGTTVTVSSGG 120

Qy        119 GGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKR- 176
              |||||||||||||||||||: :||| | :||:|| ||  : :|: |:| | |  |:
Db        121 GGSGGGGSGGGGSDIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRSA 180

Qy        177 ---WIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTK 233
                 ||    :  |:|:|||||||  || :||::| || |||||  :  |  ||| |||
Db        181 HTLHIY----IQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLHY-DNLHTFGGGTK 235

Qy        234 LELKRA 239
              ||||||
Db        236 LELKRA 241


RESULT 5
Q7TQM2
ID   Q7TQM2      PRELIMINARY;      PRT;   243 AA.
AC   Q7TQM2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ScFv 6H8 protein (Fragment).
GN   Name=scFv 6H8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Balb/C;
RX   MEDLINE=22853226; PubMed=12860977;
RA   Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT   "scFv single chain antibody variable fragment as inverse agonist for
RT   the beta-2 adrenergic receptor.";
RL   J. Biol. Chem. 278:36740-36747(2003).
DR   EMBL; AJ574851; CAE00495.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   243 AA;  25976 MW;  BEFFF64D2DCF4F76 CRC64;

  Query Match            40.6%;  Score 658;  DB 2;  Length 243;
  Best Local Similarity  53.1%;  Pred. No. 4.7e-40;
  Matches  127;  Conservative   43;  Mismatches   63;  Indels    6;  Gaps    4;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:||:||  ||:|| | |||| |||:||::: ||||:|   :||||:  |  ||    |
Db          1 QVQLQQSGSELVRPGASVKLSCKASGYTFTTYWMHWVKQRHGQGLEWIGNIYPGSGITNY 60

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGA--YWGQGTTVTVSSGGGG 120
                :  | :  :: |   :| :: ::|| |||: :|||||       || |||:||||||||
Db         61 DEKFKNKGILTVDTSSSTAYMHLSSLASEDSAVYYCARGGRGLDVWGAGTTLTVSSGGGG 120

Qy        121 SGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-RYMNWFQQKSGTSPKRWIY 179
              |||||||||||||::||| :  | | |:|||:|| ||  :   : |:||| | :|:  |
Db        121 SGGGGSGGGGSDIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLIS 180

Qy        180 DTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQ-WSSNPLTFGAGTKLELK 237
                : | :|||:|||||||  |:|:|:|:: || ||||||| ||:   ||| |||||:|
Db        181 GATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQYWSTR--TFGGGTKLEIK 237


RESULT 6
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Q925S1
ID   Q925S1      PRELIMINARY;      PRT;   218 AA.
AC   Q925S1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MRP5 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   PubMed=11819679;
RA   Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA   Su C.;
RT   "Mechanism of exogenous nucleic acids and their precursors improving
RT   the repair of intestinal epithelium after irradiation in mice.";
RL   World J. Gastroenterol. 6:709-717(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Cui D., Zeng G., Yan X., Li X., Su C.;
RT   "Cloning of mouse genes related to repairing of intestinal epithelium
RT   of the irradiated mice by treatment with the intestinal RNA of mice of
RT   the same strain.";
RL   Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR   EMBL; AF240168; AAK43733.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     218    218
SQ   SEQUENCE   218 AA;  23013 MW;  527E4FA8F7982817 CRC64;

  Query Match            37.5%;  Score 608.5;  DB 2;  Length 218;
  Best Local Similarity  55.5%;  Pred. No. 1.7e-36;
  Matches  121;  Conservative   33;  Mismatches   55;  Indels    9;  Gaps    3;

Qy          1 MAEVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTI 60
              ||:||||:||  | :|| : ::|| |||:||:: || ||:: | |||:|: :|:: |
Db          1 MAQVKLQQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINTHSGVP 60

Qy         61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR-DYG---AYWGQGTTVTVSS 116
                ||:  ||||  | :   :| :||:::|::|||  |:| | ||    ||||||||||||
Db         61 KYAEEFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMRWDYDGGFAYWGQGTTVTVSS 120

Qy        117 GGGGSGGGGSGGGGSDIELTQSPAIMSASPGERVTMTCSASSSV-----RYMNWFQQKSG 171
              |||||||||| ||||| |||||| :: | |:| |::| || ||      :|||||| |
Db        121 GGGGSGGGGSGSGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMNWFQQKPG 180

Qy        172 TSPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSME 209
                ||  ||  ||  |||||    ||||| :|| |  ||
Db        181 QPPKLLIYAASKQGSGVPAGLLASGSGTDFSLNIYPME 218


RESULT 7
HV16_MOUSE
ID   HV16_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01783;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Ig heavy chain V region MOPC 21 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
```

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RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
RN   [2]
RP   SEQUENCE OF 17-136.
RX   MEDLINE=77100368; PubMed=401950;
RA   Adetugbo K., Milstein C., Secher D.S.;
RT   "Molecular analysis of spontaneous somatic mutants.";
RL   Nature 265:299-304(1977).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00522; AAD15290.1; -.
DR   PIR; E90809; G1MS21.
DR   PDB; 1IGC; X-ray; H=-.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW   Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     16
FT   CHAIN         17    136       Ig heavy chain V region MOPC 21.
FT   DOMAIN       115    119       D segment.
FT   DOMAIN       120    136       JH4 SEGMENT.
FT   DISULFID      38    112
FT   CONFLICT      75     78       HYAD -> DYAH (in Ref. 2).
FT   CONFLICT      89     90       DN -> ND (in Ref. 2).
FT   CONFLICT     115    115       W -> H (in Ref. 2).
FT   CONFLICT     120    120       Y -> W (in Ref. 2).
FT   STRAND        19     23
FT   STRAND        26     28
FT   TURN          30     31
FT   STRAND        34     41
FT   HELIX         45     47
FT   STRAND        50     55
FT   STRAND        61     67
FT   TURN          69     70
FT   STRAND        74     76
FT   HELIX         78     80
FT   STRAND        81     81
FT   TURN          82     83
FT   STRAND        84     89
FT   TURN          90     93
FT   STRAND        94     99
FT   HELIX        104    106
FT   STRAND       108    114
FT   TURN         118    119
FT   STRAND       125    126
FT   STRAND       130    134
FT   NON_TER      136    136
SQ   SEQUENCE   136 AA;  15071 MW;  2276A98DBDBF7016 CRC64;

  Query Match             33.0%;  Score 535;  DB 1;  Length 136;
  Best Local Similarity   87.5%;  Pred. No. 2.2e-31;
  Matches  105;  Conservative    5;  Mismatches    4;  Indels    6;  Gaps    2;

Qy          3 EVKLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYY 62
              :|:| ||||||||||||||||||||||||||||||||||||||||||||||||||||::|
Db         17 DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHY 76

Qy         63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYYCAR----DYGA--YWGQGTTVTVSS 116
              |||||||||||||||||||||||||||||| ||||||     | |  ||||||:|||||
Db         77 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYYAMDYWGQGTSVTVSS 136


RESULT 8
KV6F_MOUSE
ID   KV6F_MOUSE     STANDARD;      PRT;   107 AA.
AC   P04940;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ2-17.4.1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K00735; AAA38680.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     33       Complementarity-determining-1.
FT   DOMAIN       34     48       Framework-2.
FT   DOMAIN       49     55       Complementarity-determining-2.
FT   DOMAIN       56     87       Framework-3.
FT   DOMAIN       88     96       Complementarity-determining-3.
FT   DOMAIN       97    106       Framework-4.
FT   DISULFID     23     87       By similarity.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11561 MW;  6F694284ECFA68E6 CRC64;

  Query Match             31.3%;  Score 507;  DB 1;  Length 107;
  Best Local Similarity   90.6%;  Pred. No. 1.9e-29;
  Matches   96;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||::|||||||||||| ||:|:|||||||||||||||||:|||||||
Db          2 IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||| |||||||:||:|||||||||||||||||||||||||||||
Db         62 SGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGAGTKLELKR 107


RESULT 9
KV6H_MOUSE
ID   KV6H_MOUSE     STANDARD;      PRT;   107 AA.
AC   P04942;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ5-61.1.2.
OS   Mus musculus (Mouse).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K00739; AAA38684.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     33       Complementarity-determining-1.
FT   DOMAIN       34     48       Framework-2.
FT   DOMAIN       49     55       Complementarity-determining-2.
FT   DOMAIN       56     87       Framework-3.
FT   DOMAIN       88     96       Complementarity-determining-3.
FT   DOMAIN       97    106       Framework-4.
FT   DISULFID     23     87       By similarity.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11605 MW;  CA6C4284ECFCB550 CRC64;

  Query Match             31.2%;  Score 506;  DB 1;  Length 107;
  Best Local Similarity   90.6%;  Pred. No. 2.2e-29;
  Matches   96;  Conservative    6;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | ||||||||||||||::|||||||||||| ||:|:||||||||||||||||||| |||||||
Db          2 IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLDSGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||| ||||||:||:||||||||||||||||||||||||||||||
Db         62 SGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGAGTKLELKR 107


RESULT 10
KV6I_MOUSE
ID   KV6I_MOUSE     STANDARD;      PRT;   107 AA.
AC   P04943;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ6-8.3.1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K00740; AAA38685.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     33       Complementarity-determining-1.
FT   DOMAIN       34     48       Framework-2.
FT   DOMAIN       49     55       Complementarity-determining-2.
FT   DOMAIN       56     87       Framework-3.
FT   DOMAIN       88     96       Complementarity-determining-3.
FT   DOMAIN       97    106       Framework-4.
FT   DISULFID     23     87       By similarity.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11572 MW;  6F694824ECF0C8E6 CRC64;

  Query Match             30.9%;  Score 502;  DB 1;  Length 107;
  Best Local Similarity   89.6%;  Pred. No. 4.3e-29;
  Matches   95;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | ||||||||||||||::|||||||||||| ||:|:||||||||||||||||||| |||||
Db          2 IVLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGXPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||| ||||||:||:||||||||||||||||||||||||||||||
Db         62 SGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGAGTKLELKR 107


RESULT 11
KV6G_MOUSE
ID   KV6G_MOUSE     STANDARD;      PRT;   107 AA.
AC   P04941;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ2-48.2.2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K00737; AAA38682.1; -.
DR   HSSP; Q91W12; 1AY1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
```

```
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     33       Complementarity-determining-1.
FT   DOMAIN       34     48       Framework-2.
FT   DOMAIN       49     55       Complementarity-determining-2.
FT   DOMAIN       56     87       Framework-3.
FT   DOMAIN       88     96       Complementarity-determining-3.
FT   DOMAIN       97    106       Framework-4.
FT   DISULFID     23     87       By similarity.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11556 MW;  72488DA9EF354934 CRC64;

  Query Match             30.8%;  Score 500;  DB 1;  Length 107;
  Best Local Similarity   89.6%;  Pred. No. 6.1e-29;
  Matches   95;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||::||||||||||| ||:|:||||||||||||||||||:|||||||
Db          2 ILLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              ||||| |||||||:||:||||||||||||||||||||||| |||
Db         62 SGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGAGTKLXLKR 107


RESULT 12
Q8K1F0
ID   Q8K1F0      PRELIMINARY;      PRT;   112 AA.
AC   Q8K1F0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-VIPase light chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA   Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF516285; AAM64203.1; -.
DR   PIR; A33933; A33933.
DR   PIR; PC4405; PC4405.
DR   HSSP; P01837; 1ORQ.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11901 MW;  F6644663201AA239 CRC64;

  Query Match             30.7%;  Score 498;  DB 2;  Length 112;
  Best Local Similarity   88.8%;  Pred. No. 8.9e-29;
  Matches   95;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        135 LTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARFSG 194
              |||||||||||||:|||||||||| ||:|:||||||||||||||||:|||||||||
Db          4 LTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARFSG 63

Qy        195 SGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
              |||| |||||||| | |||||||||||||| ||| |||||:||| |
Db         64 SGSGNSYSLTISSTEGEDAATYYCQQWSSNPPTFGGGTKLEIKRADA 110


RESULT 13
KV6J_MOUSE
ID   KV6J_MOUSE     STANDARD;      PRT;   107 AA.
AC   P04944;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-VI region NQ5-78.2.6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83271467; PubMed=6877353;
RA   Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT   "mRNA sequences define an unusually restricted IgG response to 2-
RT   phenyloxazolone and its early diversification.";
RL   Nature 304:320-324(1983).
CC   -!- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K00744; AAA38689.1; -.
DR   HSSP; Q91W12; 1AY1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin V region.
FT   DOMAIN        1     23       Framework-1.
FT   DOMAIN       24     33       Complementarity-determining-1.
FT   DOMAIN       34     48       Framework-2.
FT   DOMAIN       49     55       Complementarity-determining-2.
FT   DOMAIN       56     87       Framework-3.
FT   DOMAIN       88     96       Complementarity-determining-3.
FT   DOMAIN       97    106       Framework-4.
FT   DISULFID     23     87       By similarity.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11611 MW;  A38290781F3C30D3 CRC64;

  Query Match             30.5%;  Score 494;  DB 1;  Length 107;
  Best Local Similarity   87.7%;  Pred. No. 1.7e-28;
  Matches   93;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||::||||||||||| ||:|:||||||||||||||||||:|||||||
Db          2 ILLTQSPAIMSASPGQKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF 61

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKR 238
              |||| |||||||:||:||||||||||||||||||||:||||| ||
Db         62 XGSGSATSYSLTITSMQAEDAATYYCQQWSSNPLTFGSGTKLEXKR 107


RESULT 14
Q91W12
ID   Q91W12      PRELIMINARY;      PRT;   235 AA.
AC   Q91W12;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC006643; AAH06643.1; -.
DR   PDB; 1AY1; X-ray; L=23-232.
DR   PDB; 1HQ4; X-ray; A/C=23-235.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  26021 MW;  5FC73BDEBD5E8FEF CRC64;

  Query Match             30.3%;  Score 491;  DB 2;  Length 235;
  Best Local Similarity   87.2%;  Pred. No. 7e-28;
  Matches   95;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||||||||||||||| :|:|:|||||||||||||| ||:|||| ||
Db         24 IVLTQSPAIMSASPGERVTMTCSASSSVSHMHWYQQKSGTSPKRWIYDTFKLTSGVPDRF 83

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
              |||||||||||||:||||| ||||||||| || ||| |||||||||  |
Db         84 SGSGSGTSYSLTISNMEAEDVATYYCQQWSRNPPTFGVGTKLELKRADA 132


RESULT 15
Q8VDD0
ID   Q8VDD0      PRELIMINARY;      PRT;   134 AA.
AC   Q8VDD0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-MOG Z12 variable light chain (Fragment).
GN   Name=anti-MOG kappa;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Sembi P.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chernajovsky Y.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416331; CAC94866.1; -.
DR   PIR; G27887; G27887.
DR   HSSP; P01834; 1MIM.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     134     134
SQ   SEQUENCE   134 AA;  14525 MW;  CFDF8E2236E2D0CF CRC64;

  Query Match             29.8%;  Score 483;  DB 2;  Length 134;
  Best Local Similarity   86.2%;  Pred. No. 1.4e-27;
  Matches   94;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        133 IELTQSPAIMSASPGERVTMTCSASSSVRYMNWFQQKSGTSPKRWIYDTSKLSSGVPARF 192
              | |||||||||||||||:||||||||||: ||:|:||| |||||||||||||:|||||||
Db         24 IVLTQSPAIMSASPGEKVTMTCSASSSISYMHWYQQKPGTSPKRWIYDTSKLASGVPARF 83

Qy        193 SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLELKRAAA 241
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Db         84 SGSGSGTSYSLTISSMEAEDAATYYCHQRSSYPWTFGGGTKLEIKRADA 132


Search completed: December 30, 2004, 15:54:50
Job time : 190 secs
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